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AL050283 Homo sapi
AX008143 Sequence
AY008763 Homo sapi
AL834294 Homo sapi
AL834294 Homo sapi
AL834294 Homo sapi
AR08764 Mus muscu
AC126239 Felis cat
AC126239 Felis cat
AC126239 Felis cat
AC12623 Homo sapi
AC009234 Homo sapi
AC009294 Homo sapi
BC008589 Homo sapi
BC008589 Homo sapi
AC016876 Homo sapi
AC016876 Homo sapi
AC129071 Pan trog1
AC129071 Pan trog1
AC1296786 Papio cyn
AC119115 Rattus no
AC19115 Rattus no
AC197861 Rattus no
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AC126237 Canis fam
AC098923 Rattus no
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AC103148 Re
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AY008763
HSM805332
AF134031
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-MODEL-framet-p2n.model -DEV=xlp
-MODEL-framet-p2n.model -DEV=xlp
-MODEL-framet-p2n.model -DEV=xlp
-O=/Cgn2_1/USFTO_spool/US09848852/runat_16122002_132040_19132/app_query.fasta_1.519
-O=/Cgn2_1/USFTO_spool/US09848852/runat_16122002_132040_19132/app_query.fasta_1.519
-OB-GenEmbl -QFWT=fastap -SUFFTX=rge -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -TRR_MIN_INCN-15 -MODE-LOCAL
-USER-US08448852_eCGN_1_1 3637_erunat_16122002_132040_19132 -NCPU-6 -ICPU-3
-NO_KLPXT -NO_MANP -LARGEGUERY -NGG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                   December 16, 2002, 20:17:55 ; Search time 3156 Seconds (without alignments) 3061.512 Million cell updates/sec
                                                                                                                              1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV
                                                                                                                                                                                                                                      4109280
         GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                 - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemanne@dkfz-heidelberg.de;
sequenced by AGOMA (Berlin/Germany) within the Clone Robers
consortium of the German Genome Project.
This clone (DKFZDSEK0919) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/CDNA/.
   HSMBUU198 1782 bp mRNA linear PRI 10-MAR-2001
HOMO Sapiens mRNA; CDNA DKFZp586K0919 (from clone DKFZp586K0919);
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQSYORMPGNAMYRGFRVAYŘRHVLTMDDLGTLYGONNLNDOMNNYGDLVMDTVPEK
VHFPNSFFYDKLRTKGYDGYKRWTKNYDIFNKELLIPIHLEVHWSLISVDVRRRTIT
FYSORTLINTRCPKHIAKYLQAEAVKKDRLDFHQGWGYFKMNVARQNNDSDCGAFVL
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/tissue_type="uterus"
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204. .1319
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GFGGOSGPEGERSLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQ
HSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQGEFSTPSRKGLVLQL
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl, S., Ansorge, W., Deccher, M., Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Koehrer, K., Strack, N. Mewes, H.W., Ottenwaelder, B., Obermaier, B., Tampe, J., Heubner, D., Wambutt, R., Korn, B., Klein, M. and Poustka, A. Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human CDNAs
                                                                                                                                                                                                                                                                                                                                                                      Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="DKFZp586K0919"
/note="similarity to S.pombe SPBC19G7.09"
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/protein_id="CAB43384.1"
/db_xref="G1:4886467"
/db_xref="SPTREMBL:Q9Y3W9"
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204. .1319
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MetTyrSeralaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2206)
Gong,L. and Yeh,E.T.
Composition and methods relating to senpl - a sentrin-specific
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Board of Regents, The University of
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AX081143 2206 bp
Sequence 9 from Patent W00109292.
AX081143 GI:13170039
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DAPPRAGEDGRAPPQVPSPCCRPDSPRGGPSPRLGLIGALMABDGVRGSPPVPSG
PPMEEDGLRWTPKSPLDPDSGLLSCTLPNGFGGSGPEGERSLAPPDASILISNVCSI
GDPVAQLEFFGGSBLGAREABRGBERGAGANPDLASEBUTVCVGSLIDEFLQTTGSLIPL
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LGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDI
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Gong, L. and Yeh, E.T.
Direct Submission
Submitted (04-OCT-2000) Institute of Molecular Medicine, University
of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030,
USA
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Homo sapiens sentrin/SUMO-specific protease (SENP3) mRNA, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yeh,E.T., Gong,L. and Kamitani,T.
Ubiquitin-like proteins: new wines in new bottles
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    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/product="SUMO-1 specific protease 3"
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Homo sapiens SUMO-1 specific protease 3 (SSP3) mRNA, complete cds.
AF199459
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1 (bases 1 to 2258)
Choi,S.J., Jeon.Y.J., Kim,K.I., Nishimori,S., Suzuki,T., Uchida,S., Shimbara,N., Tanaka,K. and Chung,C.H.
Direct Submission
Submitted (28-OCT-1999) Molecular Biology, Seoul National University, Shillin-dong san 56-1, Seoul 151-742, Korea
1617 TGTGGCCAGGCAGAGATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGCA 1676
                                                                                                                                                   1677 TCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGACATGCCCAAACTTCGTCGGCA 1736
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/db_xref="taxon:9606"
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/codon_start=1
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Homo sapiens
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German

Cancer

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/product="hypothetical protein"
/product="hypothetical protein"
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/db_rref="G1:21739884"
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GGGFGPDPGSGTTVPARRLEPVPRPSFDASASEEEEEEEEEEDEDEEEEVAAWRLPPRW
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LAHPKNHLSPQGGGATPQVPSPCCRFDSPRGPPPRLGLLGALMAEDGVRGSPPVPSG
PPWEEDGLEWTPKSPLDPSGLLGCTPLPNGFGGQSPEGERGLAPPDASILISHVCSI
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LGTLYGQNWLWARQDLWMDYVPEKVHFFNSFYDKLFTKGYDGVRRFRVNVDI
FNRELLLIPHLEVHWSLISYDVNRRPTITYPDSQRTLMRRCFKHIAKTUADABAWKRRR
LDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKE
                                                                                        This clone (DKFZp762A152) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                /tissue_type="melanoma (MeWo cell line)"
/clone_lib="762 (synonym: hmel2). Vector pSportl; host
DH10B; sites NotI + SalI"
                Clone from S. Wiemann, Molecular Genome Analysis, German Canc
Research Center (DKF2); Email s. WiemannGdKfz-heidelberg-de;
Sequenced by BMF2 (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the
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   Submitted (09-JUL-2002) 1, D-85764 Neuherberg,
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Conservative:
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Indels:
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78. 1802
/gene="DKF2p762A152"
/note="partial similarity to protease (Homo sapiens)"
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/db_xref="taxon:9606"
/map="17"
/clone="DKFZp762A152"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2269)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
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                                                             SArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIleHisLe
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                                             sAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAs
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Nishida,T., Tanaka,H. and Yasuda,H. A novel mammalian Smt5-specific isopeptidase 1 (SMT3IPI) localized
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 983 AGCCGGCCAGCACACCCCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGGA 1042
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                                                                                                                                                                              uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa
                                                                                                                                                                                                                                                             sArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIleHisLe
                                                                                                                                                                                                                                                                    1403 AAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCATCCACCT
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                                                                                                  nLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAl
                                                                                                                                       140 aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe
                                                                                                                                                                                                                    180 lHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in the nucleolus at interphase
Eur. J. Biochem. 267 (21), 6423-6427 (2000)
20485517
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WKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMFKLRRQIYKEELCKL
                                     of
                                       Tokyo University
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Nishida,T., Tanaka,H. and Yasuda,H.
Direct Submission
Submitted (13-OCT-1999) School of Life Science, Tokyo Universi
Pharmacy and Life Science, 1432-1 Horinouchi, Hachioji, Tokyo
192-0392, Japan
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Mismatches:
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Matches:
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1. 1707
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Gong,L. and Yeh,E.T.
Direct Submission
Submitted (04-00T-2000) Institute of Molecular Medicine, University
of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                     AY008764 21-NOV-2000 Mus musculus sentrin/SUMO-specific protease (SENP3) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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nValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHi
                                    lHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLy
                                                                        sArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIleProIleHisLe
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Yeh.E.T., Gong, L. and Kamitani, T.
Ubiquitin-like proteins: new wines
Gene 248 (1-2), 1-14 (2000)
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52. .1758
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Matches:
Conservative:
Mismatches:
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                   2527: contig of 2527 bp in length
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5399: gap of unknown length
7601: contig of 2204 bp in length
7701: gap of unknown length
1701: gap of unknown length
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101268: contig of 38037 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.07e-84
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22.51%
22.30%
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9909
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
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1 (bases 1 to 139405)

8 Akhter. N. Antonellis, A., Ayele. K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., Legaspi, R., Madrov, C.L., Maduro, V. B., Marquiles, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stautrippp, S., Thomas, J. W., Thomas, P. J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC126239 139405 bp DNA linear HTG 04-JUL-2002
Felis catus clone RP86-474H17, WORKING DRAFT SEQUENCE, 12 unordered
                               1659 CTGGCCCTGTCTCAGCCATTCAGCTTCAGCCAGCAGGACATGCCCAAACTCCGTCGTCG 1718
       240 pSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyrLeuGlnAlaGl 260
                                                                                                     uAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAs 280
                                                                                                                                                                                                                                                                                        sLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGl 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (04-UUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 7.22x in Q20 bases; agarose-fp
Quality coverage: 6.57x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid, n/a; 100% of reads Sequencing vector: plasmid, n/a; 100% of reads Chemistry: Der-terminator Big Dys; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 13102% bases at least Q40 Consensus quality: 13257 bases at least Q30 Consensus quality: 13357% bases at least Q20 Insert size: 126000; agarose-fp Insert size: 138305; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 474H17
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green, E.D.
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                                                                                                260
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TITLE
JOURNAL
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REFERENCE
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AC126239
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KEYWORDS
SOURCE
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1107 others
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Conservative:
Mismatches:
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66344. 101268
/note="assembly_fragment"
101369. 139405
/note="assembly_fragment"
a 36788 c 37913 g 31272 t
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36042. .47449
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47550. .66243
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12624. 16221
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16322. 24505
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1. 2527
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Location/Qualifiers
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οý	1	MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuA	20
Dp	29569	CTGTACTCTTCCCAATGGCTTTGGGGGACCACTGGGCCAGAAGGGGAGGAGGGCCTGGC	29628
Qy Db	20	aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl	40 29688
Oy Dp	40	nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy 	60 29748
Qy Db	60 29749	salaglyglnHisSerProLeuargglugluHisValThrCysVal	75 29808
οy	75		75
qq	29809	CCAGACGGCCCGGGCCTTCTCTTCTCTCATCCAGCTCCTAAGTTGGAGTGTGGAGGCCTCA	29868
Qy Db	76,29869	GINSerIleLeuAspGluPheLeuGlnThrTyrGlySe CACGCTCCTTCCTCTCACACGC-ATCTTGGATGAATTCCTTCAGACTTACGGCAG	88 29927
Qy Db	88 29928	rLeuileProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGlnGlnGl 	108 29987
οy	108	uPh	113
q	29988		30047
δy	113		113
g	30048	CTGAGGGGCCCTAGGGGTCAGGGGTCGGGAGAATGCTGCCCAGAGGGACCGACGCAGG	30107
ογ	113		113
рр	30108	GGAGGAGGAGGAGCAGGGACCGAGGGAGGAATCTGCAGGTGAAGCGCGAAGCCCCTG	30167
δ	113		113
qq	30168	TAAGCAGATGGGGGGGGGTCCTTCCCCGGGCCCCTGAAATATGCCCCGGTGCTCACGTGCCT	30227
δý	113		113
QQ	30228	CCTTCCAAGGAGGGGCCCTTCAGCAGGCCCTCGGAAGGCTACGCGAGGCCCCGACGGGGA	30287
δy	113		113
QQ	30288	CTAGTTGAGACAGATCCTGCTTCTGGGCAGTAGAAGGTCCTTCTGTATGCCCTAGCCCCC	30347
οy	114	ArgLySGlyLeuValLeuGlnLeuIl	122
qq	30348		30407
QY Db	122	eGlnSerTyrGlnArgWetProĞlyAsnAlaMetValArgGlyPheArgValAlaTyrLy 	142 30467
ΟY	142	SArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnA	162
g	30468	GCGGCACGT	30527
ΩŸ	162	pGlnVal	164
QQ	30528	LIII CCAGGT-GAGGAGGAGGAGAAAACGGGCCCCCGAAGGGGATGTGGGGGAGCAGGGTGTCTGG	30586
οy	164		164
ор	30587	GGCCCTCTGCTCGGGGGAGCCCTGTGCCCATGCTGCGCCCTCCATGGCAAGTTGCCGCCC	30646
ò	165		179

q	30647	GTCTTCTCCCCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACGGTCCTGAAAA	30706
Οy	179	sval	180
QQ	30707	  GGT-AGGCCTGACAGGGTACTTCAGTCCCCAGGAGAACTTCTGCAGATCCCAGCAGCTTT	30765
δý	180		180
qq	30766	TGCACTCCCTTTGATCTCTTCCTTTTCATGGAGGGAGGATCTTTGTTTG	30825
δÿ	180		180
qq	30826	GGTAAAAGGCGGTCTGTTAAATTCAAACCTGTAACCTAGGTCCTGAACTTCTCTGTTCCT	30885
Οy	180		180
qq	30886	TTCCCCCCCAGTCGGCAGTGGTTCTCCCTGTGGCTCACCCCCACCAGTTGGGAGGGGCCAGCA	30945
Οy	180		180
qq	30946	GGAAGAATTGGGTTTCTGCCCCCAGTGGATTGCAGTGGAGGTTGTTGAAACTGGCCCT	31005
δŽ	180		180
QQ	31006	TGGAGCCCCAGTGACATGGAGCGGACTGGGCGGAGGAGCTTGGCAGGGAGGCCTGAAGC	31065
Qy	181	HisPhePheAsnSerPh	186
qq	31066	TCTTTTAACTCCATCCAGCTCTTTTGTGTCATTGGCACAGGTGCATTTCTTCAACAGTTT	31125
Qy	186	//AspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThr	205
Dp	31126	GATGG	31185
δy	205		205
q	31186	GAGTTGCCAGTTCACGTGTATGTGGGTAACGCCTTGCCTGTAAAGGATTAGAGTTCCGCT	31245
Qy	205		205
qq	31246	TTCTAGGAGTCCCTTCCCTGAGGCTGCTCACTCAGTCTTTCAAGTAACATGGGTCTTCTG	31305
Qy	205		205
qq	31306	TGTGTTCGGTACTGTCGTGGGCAGCAAGGACTCGGTGTTAAGTAAG	31365
Qγ	205		205
Ω	31366	TTCGTGGAGTGTGAATAAGTAAAGTTAAAATTTCAGCTAGCGTTAGGCGCCGTGAACAATT	31425
Qy	205		205
qq	31426	AAAAGGGAGATGTAGTAGCGTGGAATGTGGGTGGCTCCGGGAAGGCCCACTCTTCTCTGAG	31485
δy	205		205
Dp	31486	CCTGGAATGACGAGGGCCCGGTCACGTGTGGCTCGGGGGCAAGAGTGGTTTAGGCGAAGG	31545
δy	205		205
qq	31546	GGACGCCGAGTACGTGGGACACAAGGTGAGACTGGGGGGGG	31605
δy	205		205
QQ	31606	TGTCTGGTGTGGGGGGGGGGGGGGGGGGAATATGATCAGAAGCTTGGCCAGGGC	31665
δy	205		205
q	31666	TGATCGCGTGGGGCGTGGAGGCCGCCGTCACCGTGTGCGCTGAGGCGCCCGTTGACGAGCC	31725
Qy	205		205

TTAAGCAGGCTGGGAAGAGCCTCCTGTTTTGACGGAGATTGGAAGTGGGCCAAGATTG  AGCAGGGGACTAACTAAGAGGAAAGAGCGAAGAGGGGGAAGAGTGGATTG  TGAGGGAGGACGAGGAGGGGAAGAGGGAAGAGGGGGAACCGAGGATTG  TGAGGGAGGAGGAGGGCTCTCTGTGCGGAATTTGGAGGTGATGACTTTT  TGAGGGAGGACTAACTAGATTCCTAGGAGAACATTTGGCGAGGGGAAAAGTTTGT  GCAGAGCGTTACTTGGAATTCCTAGGAGAAAATTTTCTACAGTGAGGTAGGACTTTG  TGAGGGCTGCTGCCCTGCAATTCCTAGGAGACCTACAGTGAGGTAGGACCTTGC  TGGCAGCCTTGCTCCCGGCAATTCCTAGGAGACCTACAGTGAAGTTGCCTAGGACCTTTGCTGAGACTTTGCTGCCCTTGCCTAGAATTTCTACAGTGAGGAAATTTCTACAGTGAGACTTGGCCTTGC  TGGCAGCCTTGCTCCCGGCAATTCCTGCCCCTTCCGGGAAATTTCTACAGTGAGTTGGCTTTGCTTGC
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1 MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl 20
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                78984: contig of 10205 bp in length 79084: gap of unknown length 93446: contig of 14362 bp in length 93546: gap of unknown length 102175: contig of 8629 bp in length 131685: contig of 29410 bp in length 131685: contig of 29410 bp in length 131785: gap of unknown length 131785: contig of 29410 bp in length 131785: contig of 2943 bp in length 161428: contig of 29643 bp in length.
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  unknown length
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                                                                                                                                                                                                                                                          /organism="Canis familiaris"
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1. 4734
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4835, 7325
/note="assembly_fragment"
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41863 c 41233 g 37340 t
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Matches:
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131786. .161428
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102276. .131685
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880.00
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79085
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                   FEATURES
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                                                                                                Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Carnivora; Fissipedia; Canidae; Canis.

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 161428)

Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakseley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,

McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,

Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,

Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (10-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 148712 bases at least Q40 Consensus quality: 151471 bases at least Q30 Consensus quality: 151471 bases at least Q30 Insert size: 152000; agarose-fp Insert size: 160028; sun-of-contigs Quality coverage: 5.36x in Q20 bases; sum-of-contigs Quality coverage: 5.10x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4734: contig of 4734 bp in length
4834: gap of unknown length
7325: contig of 2491 bp in length
7425: contig of 2491 bp in length
12261: contig of 4836 bp in length
12361: gap of unknown length
19031: contig of 6670 bp in length
19131: gap of unknown length
27849: contig of 8718 bp in length
27849: gap of unknown length
31801: contig of 3852 bp in length
31801: contig of 3852 bp in length
40781: contig of 8880 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ength
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------- Project Information
Center project name: cwp
Center clone name: 332211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 9267 Egap of unknown l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown contig of 8902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Summary Statistics
                                      AC126925.1 GI:21724102
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- Genome Center
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unordered pieces.
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4835
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59151
59251
                ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
REFERENCE
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JOURNAL
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                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                AUTHORS
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Qy Dp	87138	) salaglyginHisSerProLeuArgGluGluHisValThrCysVal 75 	98
δŏ	75		179
qa	87078	3 CTAGAGGACCCAGTCTTGCTTAGTAGCCAACTCCTAAGTTGGAATCTGGAGGCCTCAC 87019	82
O <sub>Y</sub> Db	76 87018	;	Qy 179Db 85939 ITCATCCATAAAGAGGATCTTGGTTTTGG
Qy B		rLeulleProLeuSer                 CCTCATCCCTCTTAGC	Qy 179
S B S	108	uPheSerThrProSer	Oy 179Db 85819 GAGGGAGAGTGGGGGGGGAAGGCAGGAAAT
δy			179
qa	86839	GAGAGTATGGAGGTTGCTGCTGCTTTTCTCCCATAGGGATGTACAAGGCGGATGGAG 86780	8
Qy	113	113	179
qa	98	) GAAGGTAGAACTGAGGGGGAGGAACCTGTAGGCAGAGTGCCACGCCCCTGTAAACTGACT 86720	DD 85099 CCCCAGCCGAAACCAAGGCTCAGGCACTC
Óγ	113	113	8
d d	86	) GGGGTGGAGTCTTTACCTGAGATCCTGCAATATTATGTATACCTGATACTCCTGTGCCTC 86660	179
δλ	113	113	00
qa	86659	) TCTGGAGACTAGGCCTTTAGCAGGTCCTCAAAAGGATGTGTGGCCCCAAAGAAAG	179
οy			8
ති ද	8659	TTTTTGTTTGAAGTGGGTTCCACACCCAGTGTGAAGCCCCAACACAGGGCTTGAACTCACG	179
Š í			Db 85459 GAAGCAAGCGCCAGGGTGGAGGGACCT
<u>a</u>	8	ACCTTGAGATCAATACCTGAGCTGAGATCAGGAATGGGATGTTTAACCGACTGGGCCACC	Qy 180Val
ò á			Db 85399 CCAGGTCTTTGTATCATTGGCACAGGTG
8 8	864/9	TAGGIGCCCCCACCCCACCCCCTATTCTTAAGAACTTAGTTTAGGTTCTT 86420	
qa	86419	ATTCTGGGCAGTAGAAAATACTTCTGTATGCTCTAGCCCCCTTGTCTCTTGTGTGTG	85339
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a a	<b>2</b> 0	CACCCTTGGCCTAGGAAGGGCCTGGTGCTGCAGCTGATCCAGTCGTACCAGCGGAT	Oy 205
ද් යු	128 86299	, tProGlykanAlaMetValArgGlyPheArgValAlaTyrLySArgHisValLeuThrwe 148 	Db 85219 CCTCAAAGCCTGCTCACTCAGTCTTTCAAC
ò	148	tAspAspLeuGlyThrLeuTyrG]vG]nAsnTrpLenAsnAsp	Qy 205
7 Q	æ		Db 85159 GTCGTAGGCACAAGGGATTCAGTGTTGAG1
δŏ	1.62		205
QQ	86179	AGAAATGGGCCCAAAAGGGGATTTAGGGAGGAGGGTGTCTGGGGCCCTCT	89
Qy	163		Db 85039 GCAGTAGCCCGGGAGCTAGGCCCTTTAGAT
අ	86119	GCCCTATACCTATGCTGCACTCTCCATGGCAAGTTGCCTCCAATTTTCTCCCCAGGTGAT	
οy	165	tAsnMetTyrGlyAspLeuValMetAspThrValProGluLys179	

QQ	86059		86000
ΟŸ	179		179
qq	85999	ACCTCAGTCCCCAGAAGCCCTTCTGCAGTTTGAAGCAGCTTTTTCAGTCCCCTTTAATCTC	85940
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Qy	179		179
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δλ	179 -		179
Dp	85699	CCCCAGCCGAAACCAAGAGTCAGACACTCAACTGAGTCACCCAGGCGCTCCTCAAA	85640
Qy	179 -		179
QQ	85639 T	TTGTAATCGTGGTCCTGAACTTACTAATTCTTTTCCCCCAGTGTAGGGTTTTTCCCTGT	85580
Qy	179 -		179
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Qy	179 -		179
qq	85519 T	TTACCCTCAGTGAGTTGGAGTTGCAGGTTATTGAAACTGGCCCTTGGAGCCCTAATGAAAG	85460
Οy	179 -		179
qq	85459 G	GAAGCAAGCGGCCAGGGTGGAGGGGACCTGGCAAGGGGGGCCTGAGCTCTTTCAGTTCCAT	85400
Qγ	180 -	ValHisPhePheAsnSerPhePheTyrAspLysL	191
qq	85399 0	CAGGTCTTTTGTATCATTGGCACAGGTGCATTTCTTCTACACAGTTTCTTCTTCTATGATAAAC	85340
Qy	191 e	euArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsn	205
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Qγ	- 502.		205
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Dp	84979 AGGTTTGAAGGCCAAGGAGCTGGCCCTGCAGATCTGGGGGAGGAGGTGGTCTAGGCAAAGG 84920		
ò	205	Qy	205
qq	84919 AGTAGCAAGTACATGGGACCCAGAGTGAGAATGAGCATTTGAGGCACCGAAGGCCCATGT	qa	83839 CATCCTGGGGTCTCA
Qy	205 205	Οy	
qq	84859 GGGTGTCCTGTATAGTTGGAGCATCTGAGTGGAGGGAGTGTAGTAAGAAATCCGGTCAGA 84800	<b>Q</b> O	83779 CCCTGGAATCTACAC
Qγ	205 205	Qy	
Q ·	84799 GTTGATCCTGTAAGGCATGGAGGAGGAGGAGGATCTTTCTT	QQ ,	83719 CCCACTGGGCTCCTT
Qy	205 205	δδ	
QQ	84739 AGCCACTGAAAAGTTTTAAGGAGCCTGGGAAGTCCCTCATGTTTTCAACTCCTGCTTCAT 84680	QQ Q	
ò	205 205	Qy	212 GluLeuLeuLeulle 
Db	84679 GTAGACTGGAAGTGGGGGGAAGAGTAGAAGCAGGCAGACTGGCCAGGGAGGG	q <sub>0</sub>	
δy	205 205	λō	232 ArgArgArgThrIle
QQ	84619 AAGCCTGGAGGGCGCTGAGTGCAGAATGGAAGTGGCTTTCTCTAGGATAGGTTTTG 84560	QQ ·	
Οy	205 205	δλ	
q	84559 TGGGTAGAACCATGGTATTTTCAGATGGGTTGGGGAATGAAGAAGAGCTAGGAAT 84500	qq	83480 GGTTTGAGAGGGAAG
QY	205 205	Οy	251
g	84499 TGGGGAGGCCTGGGTTAGTGGCAGAAGTTACTGGGGAAATGAGGGAACGCGTTTGGTGA 84440	QQ	83420 AGTGGGCAGAAGGGC
Qγ	205 205	ΟŸ	
qq	84439 TGGGGTAGGGGTAGCTTTTCTCCCCTCTAGTTGGGGTCCCTGCCCTCCCGCCAAAG 84380	Dp	
δy	205 205	Οy	260 GluAlaValLysLys
qq	84379 GTGAAAAATTGGTCTAGAGTGAAGTGGGACTGGCTCTGGCATTTTAGTTTCTGTCCCCG 84320	qa	
οy	205 205	Oy	
qq	84319 GGTTCAGGGGCTTACACCTGCAGTGACCTGGCAGGCCCGCTTCTCCCCAGTATGGGTGGG	QQ	83240 GTAAGTGTCTGGAGG
δý	205 205	ΟŊ	279
gg	84259 TAACACAGTGGAAAGAACGTGGCCTGTGTCCCTGTGTCCTTTCTCCTGTGCCCGTCAGA 84200	QQ	
δy	205 205	δō	280 -AsnvalAlaArgGI
QΩ	84199 AAGGIGCCCTACTCCCAGGCTGCAGTTCCATCGTTAGGCTGACTGA	ag .	
ΟŸ	205 205	δo	295
ДQ	84139 AGGGTGGTTGTGGTAACGGGCCCACCCTTACTAGGTCCTGTGCGGTGCTGTTAACGTAT 84080	a a	83060 AGATCGGTGGGGTTA
ΟŸ	205 205	Qy	
QQ	84079 CATGGACAGGAACTAATTTAACTCTGGTAACAAGAAGAGGAGTAGGCACTGTTATTCGC 84020	qq	83000 GCTCACAGGCACTIG
Qy	205 205	ΟŊ	295
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Qy	205 205	ογ	295
Q	83959 ACAAGCTAGGAAATGGAGGAGCTGGGTTTAAACCCCAGGGGGGGG	QO	82880 TCTGGCCCTGGTACA
ΟŸ	205 205	Oy	295
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οy	205		205
g	83839 CATCCTGGGGT	GTCTCAGGTGTGTTGTGACAGTAGGTCTTCTGACCTGCCTTCTTCCCTCAC	83780
Oy	205		205
άq	83779 CCCTGGAAT	CTACACATGCTGAACTTCACCTCACAGTGGAGGAGCTCAGCTGTGTGCTTG	83720
Qy	205		205
Dp	83719 CCCACTGGG	CTCCTTGTCTCCGCCTCCACTCTTTAGGACCCTCGCGGCAATGGGCAGGTG	83660
δŏ	206		211
g	83659 GCTCCTGCT	– to	83600
δ d	212 GluLeuLeul 	LeuLeuLeul]eProlleHisLeuGluValHisTrpSerLeulleSerValAspVal :: 	231
9	SSSS GAG	5	£00
oy D	232 ArgArgArg;           83539 AGCCGACGC	ArgkrgThrIleThrTyrPheAspSerGlnArgThrLeuAshArgArgCysProLys	251 83481
ò	251		51
q	80 G	GTTTGAGAGGGAAGGCGGGGGGGGGGGGGGGGGGGGAGAATCCAGTGGCAAGGCAT	~
ΟY	251		251
Dp	83420 AGTGGGCAG	TGGGCAGAAGGGCAGGCCTGGTGCACCACTGTACCCTAGGTTCACTTGGGAAA	83361
δy	252	æ	259
QQ	83360 CCGAGGCAT		83301
Οy	260 GluAlaVall	uAspPheHisGlnGlyTrpLysGlyTyrPheLysMet	279
QQ		TCAAAATG	83241
QY	279		279
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Óγ	279		279
qq	83180 AAGAAGTGGAAGC	CACACCCCGAGGAGCGTCCAGGTGAAGGACTTCTTTTTTTT	83121
Οy	ď.	3lyAlaPheValLeu	295
q	83120 GAACGTGGCC		83061
Οy	295		295
q	83060 AGATCGGTGC	GGGGTTAAAGGTTTGGTAAGGAGGTGGGAGGCTGTTCCACCTCTCTGGTTTG (	83001
٥y	295		295
qq	83000 GCTCACAGGC	ACTTGTGAAGCAGAGGAACCTTAGGTGTTAGTGTGCAGAAACTCGGAT	82941
δy	295		295
qq	82940 CCCCTTGGTC	CCCCTTGGTCTCCCGGGCTTCCCCGGGCCCACACTTGGCCTGGGTCTCTTGGTCCTTGGTC {	82881
δy	295		295
QQ	82880 TCTGGCCCTC	GGTACAGTTGCTTCCCAACCCCCAGTGCAAAGCATTTTCTTCAGGTATCGA	82821
δy	295		295
QQ	82820 GAACAGTGAC	GAACAGTGACTCTAGAGTCAGGCTTTGAGCCTTAGGCTATGGGACGTTGGCTTTGTGTGT 8	82761

295

82581

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartlodactyla; Ruminantia; Pecora; Bovoidea; Bovidea; Bovid

Direct Submission Submitted (10-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA Unpublished , 2 (bases 1 to 153553) Green, E.D. JOURNAL REFERENCE TITLE JOURNAL AUTHORS

TITLE

25325. .32504 /note="assembly\_fragment" 'note="assembly\_fragment" note="assembly\_fragment"

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.40970

32605.

11071. .56590

Center: NIH Intramural Sequencing Center Center code: NISC ----- Genome Center

COMMENT

Web site: http://www.nisc.nih.gov Contact: nisc\_zoo@nhgri.nih.gov ------- Project Information Center project name: ddi Center clone name: 045D24

Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 147748 bases at least Q40 Consensus quality: 14748 bases at least Q20 Insert size: 151000; agarose-fp Insert size: 15485; sum-of-contigs Quality coverage: 8.0x in Q20 bases; sum-of-contigs Quality coverage: 8.72x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

soon as it is available and the accession number will gap of unknown length contig of 16990 bp in length gap of unknown length in length of 17079 bp in length contig of 20469 bp in length of 42025 bp in length unknown length of 8366 bp in length bp in length bp in length bp in length length length length length unknown length unknown length gap of unknown length pp in of 15520 bp unknown of 7180 unknown of 9325 1. .153553 /organism="Bos taurus" /db\_xref="taxon:9913" /clone="RP42-45D24" /clone\_lib="RP42" 1. .2312 /note="assembly\_fragment" 2413. .5841 /note="assembly\_fragment" unknown unknown 2494 of 7264 5942. 8435 /note="assembly\_fragment" 8536. 15799 /note="assembly\_fragment" .5900, .25224 note="assembly\_fragment" contig gap of contig gap of contig gap of contig contig gap of contig gap of contig gap of contig Location/Qualifiers contig gap of gap of contig clone\_end:T7 vector\_side:left" 111428: 15899 26690 41070 preserved 2313 15800 15900 25225 25325 32505 32505 40971 41071 56591 73770 73870 90860 90860 5842 5942 misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature as source FEATURES

1107 others vector\_side:right" 39178 a 37393 c 36616 g 39259 t clone\_end:SP6 Alignment Scores: BASE COUNT ORIGIN

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3870.

US-09-848-852A-3 (1-332) x AC126921 (1-153553)

Conservative: Mismatches: Indels:

849.50 22.21% 21.91% 47.94%

Best Local Similarity: Query Match: Percent Similarity:

Pred. No.:

Score:

Length: Matches:

1 MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAla-HisLeuAl 20 οy us-09-848-852a-3.rge

qq	36532	:::	36473
ò	7 7	aProProAspAlaSer1leLeu11eSerAsnValCysSer11eGlyAspHisValAlaGl	0
QQ	364/2	ACCCCTGATGCCAGCATCCTCATCAGCAACGTGTGCAGCATCGGGGACCACGTC	36413
Oy Dp	40	nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy 	60 36353
ò	9	S	77
q	36352		36293
δy	77		77
qq	36292	CTCCGGGATCTCGTCTTTCCCCTCAGCTGACTGTGAGATCGGAGTCTGGAGTCTCACTTT	36233
δy	78		06
Dp	36232		36173
Qy	36172	eProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGluPheSe 	110
ò	Ξ	Thrproxer	13
: 염			36053
οy	113		113
q	36052	***こうべいしゃいつかりからない。	25003
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οy	11	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	113
Dp	35992	GCTAGAACTGAAGGGGAGGAATCTGCAGACAAGGTGCCAAGCCCCCGTGAGCCACCCGGG	35933
οy	113		113
qq	35932	AGGGCCTTTACCTGGGACCCTGAAATACCATGTGGACCTAAGTATTCCTATGCTTCTTAC	35873
δλ	113		113
QQ	35872	AGGGGAGTGTGCCTTTAGCAAGTCCTCAAAAGGACCCATGACCCAAAGAAAAGTTTTAG	35813
Qγ	113		113
QQ	35812	ATTCTTATTCTAGGCAGTAGAAGGTACTTCTGTGTGCCCAAGCCACCGCCCCGGTCCCCAA	35753
Ωy	114	ArgLysGlyLeuValLeuGlnLeuIleGl	123
qq	35752		35693
Οy	123	nSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysAr	143
qq	35692	GTCATACCAGCGGATGCCAGGCAATGCCATGGTCAGGGGCTTCCGAGTCACCTATAAGCG	35633
Q d	143	9HisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAsp	62
3	000	ecarere.	355/3
δy	162		162
qq	35572	GGTAAGGAGGTGTGGAGAAACAGGCCCCAAGAGTAGGTTTGGGGAACAATGTATTTGGGGC	35513
Qγ	162		162
q	35512	CCTCTCTCGGGAAGCCCTGTACCCATGCCACACCCTCCATGGCAAGTGGCCTCCCGTC	35453
οy	163	GlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLys	179

Q O	35452	TTCTCCTCAGGTGATGAACATGTACGGAGACCTGGTCATGGACACAGTCCCTGAAAAGGT	35393
Qy	179		179
QQ	35392 1	AGGCCTAACTAGATACTTCAGTCCCTGGAAAAACTTTTGAAGTTTTTAAGCAGCTTTTTCA	35333
QY	179		179
Dp	35332 (	GTCTCTCATGTCTTCCATTTTACGTAAAGAGGGTCTTTCTT	35273
QY	179		179
qq	35272	AGGTAATTTGTTAAATTTCAAATTTGTAATCTTGGTCCTGAACTTTTCTAGTCCTTTCCCC	35213
Qy	179		179
qq	35212' 1	TAGTCTGTAGTGTTTTTCCCCAATGGCTAGCCCCACAAATCAGGGTGGGAACTTATAAGA	35153
QY	179		179
qq	35152	TGAGGTTGAAAACAGTTTGTGCTTTTTACCTTTAGTAAGTTGGACTGGAGTTTGTGGAAA	35093
Qy	179		179
QO	35092	CCAGTCCTTAGAGCCGTGATGAAATGGACGGGGGGGAGAGACACGTGGCGGAGGG	35033
Οy	180	valHisPhepheA	184
qq	35032 (	CCTGCGGTCTGTTGATTCCACCTGGCTCTTTTGTATCGTTGGCACAGGTGCATTTCTTCA	34973
Ωy	184	snSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrL	204
Dp	34972 1	ACAGCTTCTTCTATGATAAACTCCGTACCAAAGGTTATGATGGGGGGAAAAGGTGGACCA	34913
Qγ	204	ysAsn	205
qq	34912	AAAACGTGAGTTATGAATTCACATCTTATGTAACACCTTGCCTTAAAGAAGAGTTCTGT	34853
Qy	205		205
qq	34852 1	TTCCTGTGAATCCTTTCCCCAGCTCTGTTCATTCAGACTTTCAAGTATTTATT	34793
Οy	205		205
qq	34792 1	TTTTGTGTGCCAGGTACTGTTCTGGGCATTAAGGATACAGTATTAAATAAGGAAAACTTA	34733
Qy	205		205
QQ	34732 1	TTGCCTTTTTAGGGGTGAGAATCAATAAGCCAGTTAAAGTACAGCTAGTGATAATTTGCTG	34673
ΟY	205		205
QQ	34672 9	TAAACAAAACAGTAATGTGGTAGCATGGGGCTGGGTACTTCAGATAGGGTGGTTTGGGAA	34613
ΟŊ	205		205
qq	34612 (	GGCTTCTCTTAGCTGATACTTTAGTGAGCCAGCCCTGTGCACATCTGGGCAAGGGTGTAC	34553
Qy	205		205
qq	34552 1	TAAGCAAAGGGAACACCGGGAACATGGGATACAGAGCAAGAAAGA	34493
Qy	205		205
QQ	34492 1	AGGCCCCGTGTGCCTGTGTTGGTTGGACCAGAACGAAAAAAAA	34433
oy.	205		205
qq	34432 1	ATTTGGTCAGAGAGTAGATCATGTGAGGCGTGGAGGGCAGGTCAACCAGGGTAGATTTTA	34373
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οy	205	205		47	 	
qa	34312	! TTAAACTCCTGTTTCGGCGATGGAAAGGGGGCAAGAGTGGAAGCAGGCAG	53	5		1
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qa	34252	GTAGCTGAGAAGTCCTGATGAGAAACTTGGACCAGAGTGGTCAGTGTGGAAATATTGATA 34193	93	Dp 33	33172 CT	CTCATCT
Qy	205	502				AsnArgA1
q	34192	S GTAGTAGTTTTAGGGTAGGTCCTTGCAGGTAGAACCAATAGGACTTTCTGATGGATT 34133	33			AACCGCC
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QQ	34132	GGACATGAGAGATGAGGAAAAGATAGCAATCAAGGATGATGTCTAGGTTTTTTGGCCTAAG 34073	73			ATCCAGTO
δŏ	205	302				
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qq	34012	TITCTCCATTCTGATTAGTTTACCTGTCCTCGATTCAAAGGCCAGGAAATTCCAATAGT 33953		32		CTTCTTT
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q	33952	GAGGTAGGGCTATTGCCTCTAGCATTTCTTAATTCCTGTTTCCTGTAGAGGTGGGGTGA 33893	93	Db 32		AGACCGG
οy	205	502				
q	33892	CCTGCATCGGAAAGAACTTGGCTTTCTATATGCCTGTGTCCTGTGTTTAAATTCCACCTC 33833	33	Db 32	32812 GA	GAGGTTT
· Q	205	502		ογ	280	1
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οy	205	205		AK000923	4	00004
q	33712	CATTGTTCTTAGAGTATTGTGGATATCAACTAGTTCAATCTGTGTAACAACAGGTGAGG 33653	53	DEFINITION		HOMO
QY	205	502		VERSION		AK0008
q	33652	: ATAGATACTGTTATTTTCAGTCTTACAGAAAAGAAATTGAGGTATAGAGTTACTAAGTA 33593		SOURCE		O11go Homo
Οŷ	205			ORGANISM		MKNA, Homo
đ	33592	: ACTIGCTIAGIAACCCAAGIAACITAACIAAGIAACITAGIAACCCAGGIIACTIACITA 33533	33			Eukar) Mamma]
Qy	202	205		REFERENCE AUTHORS		ı Isogai
đ	33532	: CTTGGGTCATACATGGAGGAGGTGAGGTTTGAACCTTGAGAGTCTGACTCCAGGATCTTGA 33473	73			Nishi
ΟY	205	205				Arıta, Wakama
qa	33472	: ACCTACTAAGCATTIGTACCTTTAATGIGTAAAAAGTACCTGGCCTAICCTGGGCCCICC 33413		JOURNAL		NEDO 1 Unpub]
QŸ	205	205		AUTHORS		Isogaj
QO	33412	: AGTGTTTGTTCTGTACCACCTCCTCTGTCTTGCTTTCCTCCTTAAGCCCAAGAATCCGAA 33353	53	TITLE	NAL	Submit
οy	205	205		in a joint of		(E-maj
qq	33352	: CATCCAGATGCTGGGCCTTGCCTCACGGTCCAGGGCTAGGAGTTGAGTTCTTCCACTTA 33293	93	COMMENT		Interi
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qa	33292	GCTTCTTGCCTGCTCCTCCTGTGCTATCTTACCTGACCTCCAGCCCTGCCTCCTTAG 33233	33			etc.)

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, , , , , ,	252 252 264 264 872 279 812	CTTCTTTCTCCTCCATCTACCATATTGCCAAGTATCTGGGAAGGCAGGGCAGGGCAGGAAGAA  SASPARGLEUASPPHEHISGINGLYTTPLYSGATATCTGCAGGCAGAGGCAGTGAAGAA  1	264 3287 279 3281 279 3275
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PEATURES  Location/Qualifiers  source  /organism="Homo sapiens" /organism="Homo sapiens" //db xref="texon:9606" //clone="HEMBA1001413" //tissue_type="whole embryo, mainly head" //tissue_type="whole embryo, mainly head" //tissue_type="whole embryo, 10 weeks" //dev_stage="embryo, 10 weeks" //dev_stage="embryo, 10 weeks" //force="cloning vector: pME18SFL3" //force="unnamed protein product" //codon_start=1 //codon_start=1 //protein_id="BAA91428.1" //protein_id="BAA91428.1" //protein_id="RANSNSLSISPUESLGHYYLMLMGSPFLGVGLTLVDSASVYPSCGL ICMHESTVCIPLCFPQASLSCPFHFPCPIGLLSCTLPNGFGGGGSPEGERSLAPPDAS ILISNVCSIGDHYAQELFGGSDLGMAEBAERFGEKAGQHSPLREEHYTCVQSILDEFL ORIGIN 339 a 372 c 439 g 428 t  ORIGIN	ignment Scores:  16	Db 814 GTAGTCATGTTTATCTTCTGGGGAGTGGGCCTTTCGCAGGTCCTCAGAAGGACCCATCA 873 Oy 113

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Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Luna, R., Ma, J., Mahashari, M., Mapua, P., Martin, R., Martinacle, A., Martinez, E., Massey, E., Mawhiney, E., Marchin, R., Maedor, M., Mei, G., Metzker, Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Role, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, M., Svatten, A., Tamerisa, R., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellfrod, B., Thomas, N., Thomas, S., Warten, K., Washington, C., Watlingmson, A., Williamson, A., Williamson, A., Williamson, A., Williamson, D., Wooden, S., Worley, C., Wu, Y., Wu, Y., R., Zhou, J., Zorrilla, S., Nelson, D., Prince, E., Land, C., Land, C., Land, C., Land, C., Land, C., Land, C., Martington, D., Prince, E., Land, C., Land, C., Land, C., Martington, D., Prince, E., Land, C., Land, C., Land, C., Martington, D., Prince, E., Land, C., La
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NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases I to 257644)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, 77 7030, USA On Jul 11, 2002 this sequence version replaced gi:20258090.
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
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COMMENT

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America fascicularis brain cDNA clone:QtrA-13616, full insert sequence.
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Description: 1st strand cDNA was primed with an oligo(dT) primer
Description: 1st strand cDNA was primed with an oligo(dT) primer
[ATGTGGCGTTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized
using specific 5' and 3' primers and amplified by PCR. The PCR
product was digested with Sfli and size selection was performed to
exclude fragments <1.5b. The Sfli digested PCR product was cloned
into distinct Draili sites of pME18S-FL3. xhol sites just outside
 206438 GGCGAGCTGATAATGGATGCAGTCCCAGACAAGGTCCACTTCTTCAACAGCTTTTTCCAT 206497
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                   oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to mRNA,
clone_lib:macaque brain cDNA library QtrA clone:QtrA-13616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                    206558 TITAAAAAGGTCTTCTGTTGATTCCCATCCACCTGGAGGTCCACTGGTCTCTCATTACT
                                                                                                                                                                                     229 ValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArg
                                                  189' AspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIle
                                                                                                                 PheAsnLysGluLeuLeuLeuIleProlleHisLeuGluValHisTrpSerLeuIleSer
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                                                                                                                                                                                                                                                                                                                   PheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAspSer
                                                                                                                                                                                                                                                                                                                                                  206738 TITCTICAGGGTIGGCAGACTGCTGTTACAAAGTGTATTCCACAACAGAAAATGACAGT
                                                                                                                                                                                                                                                   249 CysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAspArgLeuAsp
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
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       were constructed by oligo-capping method (Sugano et al., , Institute of Medical Science, University of Tokyo).
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can be used to isolate the cDNA insert.
                                                                                                                                                                                                                                                                                                /tissue_type="temporal lobe right"
/clone_lib="macaque brain cDNA library QtrA"
/dey_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
                                                                                                                                                                              1. .2007
/organism="Macaca fascicularis"
/db_xref="taxon:9541"
/clone="QtrA-13616"
                                                                                        Custom primer used for sequencing (5' end primer [CTGCTGCTAAAAGCTGGG]; 3' end primer [CGACCTGCAGCTGAGCACAA]).
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAR Plate: 19 Row: e Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1830)
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Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center Center code: BAM HGSC.
Center code: BAM HGSC.
Contact: http://www.hgsc.bcm.tmc.edu.
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garci
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
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981
922 TTCTACTTGAGTAGTCATGTTCTTTCTGGGCAGTGGGCCTTTCGCGGGTCCTCAGAAGGA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Homo sapiens, clone IMAGE:3448367, mRNA, partial cds.
BC008589
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TITLE
JOURNAL
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VERSION
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BC030705
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SOURCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 GlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGluLysAlaGlyGlnHisSerProLeuArgGluGluHisValThr---CysValGln 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                   /note="Vector: pCMV-SPORT6"
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                      Location/Qualifiers
                                                                                                                                                                                            /lab_host="DH10B
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789.00
73.72%
54.01%
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PRI 30-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKKQRKILWRKGIHLAFSEKWNTGFGGFKKFYFHQHLCILKAKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24 MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: RAK Plate: 33 Row: i.Column: I
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCU30705 2793 bp mRNA linear PRI 30-MAY-2
HOMO sapiens, clone MGC:27076 IMAGE:4824344, mRNA, complete cds.
BC030705
                                                                                                                                                       296
                                                                                                                    LeuGlnAlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTyr 276
                                                                                                                                                                                                                                                                                                                                                                      TyrCysLysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLys 316
ThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
                                                                                                                                                                                                                                                                                  GTTACGAAGTGTATTCCACAACAGAAAACGACAGTGACTGTGGGAGTCTTTGTGCTCAG
                                                                                                                                                                                                                                               PhelysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGln
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
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Strausberg, R.
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58 GlyGluLysAlaGlyGlnHisSerProLeuArgGluGluHisValThr---CysValGln 76 Length:
Matches:
Conservative:
Mismatches:
Indels: 716 (1-2793)ρ US-09-848-852A-3 (1-332) x BC030705 1.18e-68 789.00 73.72% 54.01% Percent Similarity: Best Local Similarity: 841 Alignment Scores: Query Match: BASE COUNT ORIGIN .. 0 ŏ g

1775 ::: ::: ||| ::||||::: 1830 TTTATCAATAGGGAAATAACAAACTATCGGGCCAGACATCAAAAATGT------AAC 1880 2120 2180 2181 TCATTTTATGATTCCCAAGGCATTCATTTTAAGTTTTGTGTAGAAGAATATAAGAAAGTAT 2240 176 ValValGluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGly 116 156 AspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIle 216 276 LeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGly 136 ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196 ProlleHisLeuGluValHisTrpSerLeuIleSerValAspValArgArgArgThrIle 236 ThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTyr 256 96 LeuGlnAlaGluAlaValLySLySAspArgLeuAspPheHisGlnGlyTrpLySGlyTyr GlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal 2121 CCTATTCACCTGGAAGTCCACTGGTCTCTTACTGTGACACTCTCTAATCGAATTATT PheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGly 2241 TTGCTGACTGAAGCCAGAGAAAAAATAGACCTGAATTTCTTCAGGGTTGGCAGACTGCT PheLysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGln 1776 117 137 157 177 197 217 6

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2301 GTTACGAAGTGTATTCCACAACAAAAACGACAGTGACTGTGGAGTCTTTGTGCTCCAG 2360

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316
TyrCysLysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLys
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Sequence

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Sequence 9, Appli Sequence 1979, Ap

Total number

Searched:

Sequence Sequence Sequence

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Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence 12 Sequence 19 Sequence 71

Sedneuce Sequence 2836, Ap 6, Appli

Sequence Sequence S

Sequence

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Run on

Sequence:

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GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Ave, N.W., Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USAN
ZIP: 20005-1934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
US-09-134-001C-1230

US-08-531-927B-8

US-08-656-005A-5

US-09-073-259-5

US-09-073-259-5

US-09-133-095-5

US-09-133-095-5

US-09-138-596-1

US-09-138-596-1

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US-08-09-013-354-6

US-08-013-055-6

US-09-013-354-6

US-09-013-354-6

US-08-01-991-99

US-08-01-991-991

US-09-01-269-32

US-09-134-011-1979

US-09-134-011-1979

US-09-107-562-28

US-09-407-562-28

US-09-407-562-28

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US-09-131-011-2836

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US-09-131-011-2836
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CORRESPONDENCE ADDRESS:
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                           - nucleic search, using frame_plus_p2n model
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US-09-356-952-12
US-09-134-001C-405
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US-08-752-929-2
US-09-534-638-1
US-08-375-709-1
US-08-752-929-1
US-09-090-793-1
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US-09-511-477-38
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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length: 2000000000
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Match
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Maximum DB seq
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Perfect score:
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAX-1992
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  US-08-375-709-2; Sequence 2, Application US/08375709; Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (22.7 TELEX: 904136
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1983 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA ZIP: 20007-5109
COMPUTER READABLE FORM:
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32.96%
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                    287 AspSerAspCys 290
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APPLICANT: YAZAWA
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Best Local Similarity:
Query Match:
DB:
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LOCATION:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal 98
                                                                                                                                                                                                                                                                                                       LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla 61
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Matches:
Conservative:
Mismatches:
Indels:
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108.00
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6.09%
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4835 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                      linear
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Best Local Similarity:
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US-08-976-259-58
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APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Biscosapentaenoic Acid
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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ORGANISM: Shewanella putrefaciens SCRC-2874 (FERM ORGANISM: BP-1625)
                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/375,709
FILING DATE: 20-JAN-1995
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53466/150/AAOK
RELEPRONGINICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
                                                                                                      STREET: 8000 K Street, N.W., Suite 500 CITY: Washington
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1422 TGTTGCAACGCCATTAAATAAGGTGGTGATGGCCGAGCCAGAAAATGACTCC 1473

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GENERAL INFORMATION:
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAMADA, Akiko
APPLICANT: XAMADA, Akiko
APPLICANT: KATO, Selashi
APPLICANT: KONDO, KIYOSI
TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
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REFERENCE/DOCKET NUMBER: 53466/150/AAOK
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JRN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MA-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 4-147945
FILING DATE: 15-MA-1992
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, HAIOLD C.
                                                                                                                                                                                                                                                                                                                                                                                    ZIE: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        Sequence 2, Application US/08752929 Patent No. 5798259
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1983 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                Foley & Lardner
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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(202)672-5399
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FEATURE:
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ORGANISM:
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                                      GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl
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                                                                                                28 eSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAspLe
                                 GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl
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GENERAL INFORMATION:
APPLICANT: Brandt, Annika
APPLICANT: Brandt, Annika
APPLICANT: Brandt, Annika
APPLICANT: Brandt, Annika
APPLICANT: Westerlund, Johanna
TITLE OF INVENTION: Promoter for Neuropeptide FF Promoter and use thereof
TITLE OF INVENTION: For therapy and diagnosis
FILE REFERENCE: 2330-104
CURRENT APPLICATION NUMBER: US/09/534,638
CURRENT FILING DATE: 2000-03-27
EARLIER FILING DATE: 1999-08-03
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
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Mismatches:
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US-09-534-638-1/c
; Sequence 1, Application US/09534638
; Patent No. 6320038
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 9840
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
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 6657 GGACCACTTTGGCGGGGTCTTCCAAGAGATGTTCCCTGATGTCAAAAGTCTACGG 6716
                                                                     -----GATAACATCACTAAAGAAATTGTCGATGAGAACGTACT 6758
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CTATCAAGGTATGCACAACATTTATACGCTGCGCGGCGCTAAAGTACGTGATGCGCTCAA 7097
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                                        eSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAspLe
                                                                                                             uGly-------MetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHi
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US-08-752-929-1
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                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl 28
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75
43
117
123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION UNDBER: JP 4-147945
FILIG DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/375,709
FILING DATE: 20-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                 Sequence 1, Application US/08375709
Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 5346
TELECOMMUNICATION INFORMATION:
TELEPAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                         Kazunaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 37895 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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20.95%
5.25%
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APPLICANT: KATO, SEISHİ
APPLICANT: KONDO, KİYOSİ
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & I
                                                                                                                                                                                                     APPLICANT: YAZAWA, APPLICANT: YAMADA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20007-5109
                                                                                                                                                                                      GENERAL INFORMATION:
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Query Match:
DB:
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                                                                        GAT 3237
                                    Asp 268
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Sequence 1, Application US/09090793
Patent No. 6140486
GENERAL INFORMATION:
APPLICANT: Calgene, LLC
APPLICANF CAIgene, LLC
TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression TITLE OF INVENTION: of polyketide-like synthesis genes in plants
FILE REFERENCE: CGNE.131.01US
                                                                                                               6879 CGTCGCCCCA----GACTACACCTTAAACAGTGAAGGCAAATGGGAAACGCTGACG-- 6930
                                                                                                                                                                                                                                                                                                       ------ATTGATGGTCTAGAGATGGTGTTTATGGATGCCTCGGGCACCGAAGCTGA 6980
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                                           6759 TGCCGGTAACGCCATGAGCCGCCGCGCGCAGCTTATCAATACGGCGCAACACTGGGCAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 IMetAspAspLeuGlyThrLeuTyrGlyGln-----AsnTrpLeuAsnAspGlnVal--
  --- MetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHi
                                                                                      ----SerProLeuArgGluGluHisValThrCy
                                                                                                                                                                          74 sValGlnSerIleLeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerTh
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                                                      APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Seishi
APPLICANT: KATO, Seishi
TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Enzymes and Process for Production of Eiscosapentaenoic
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl 28
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                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53466/150/AAOK
                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY AAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 5346/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 1-1.
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 37895 base pairs: TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8
93.00
32.96%
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                                        YAZAWA, Kazuna
YAMADA, Akiko
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20007-5109
                    GENERAL INFORMATION:
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Patent No. 5798259
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COUNTRY:
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6657 GGACCACTTTGGCGGAGCTCGCGGTGTTCAAGAGATGTTCCCTGATGTCAAAGTCTACGG 6716
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------ATTGATGGTCTAGAGATGGTTTATGGATGCCTCGGGCACCGAAGCTGA 6980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 ------AsnAlaMetValArgGlyPhe-----ArgValAlaTy 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 rMetAspAspLeuGlyThrLeuTyrGlyGln-----AsnTrpLeuAsnAspGlnVal-- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 -MetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysValHisPhePheAs 184
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                                                                                                                                                                                                                                                                                                                                      GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DARE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.0
                                                                                                                         ; TYPE: DNA
; ORGANISM: Shewanella putrefaciens
US-09-090-793-1
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Best Local Similarity:
                                                                                                         LENGTH: 37895
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                                                                                                                                                                                                     Pred. No.:
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QQ	Db 7371 TAACGCTAAAGCGGTTTATAACAAGTATCTA	7401
οy	223 sTrpSerLeulleSerValAspValArgArgArgThrIleThrT	Ar 243
QQ	Db 7402GCTACTTCGATATGAACCC	CC 7421
ΟY		7
Q	7422	GG 7481
οy	Qy 259AlaGluAlaValLySLySAspArgLeuAspPheHisGlnGlyTrpLySGlyTy ::        :::	
QQ	7482	TT 7541
οy	Oy 276 rPheLysMetAsnValAlaArgGlnAsnAspSer 288	
QQ	7542	
RES US-	SULT 8 -09-302-812-38/c	
 ญ घ (	; Sequence 38, Application US/09302812B ; Patent No. 6333148	
 	; GENERAL INFORMATION: ; APPLICANT: JACOBSON, Myron K.	
	; APPLICANT: JACOBSON, Elaine L.; APPLICANT: AM, Jean-Christophe	
· · · ·	APPLICANT: LIN, Winston TTILE OF INTERNAL DOLV/AND-PIBOSEN	HYDROLASE /I
	TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND TITLE OF INVENTION: THEREMITH	ANTIBODIES IMMUNO
	FILE REFERENCE: NIAD 201 · COO 2202	
	CURRENT FILING DATE: 1999-04-30	
	; EARLIER APPLICATION NOMBER: 60/083,768 ; EARLIER FILLIO DATE: 1998-05-01	
 	; SEQ ID NOS: 38	
	LENGIH: 29/93 TYPE: DNA	
; ;	. OKGANIAM: Caenornabaditis elegans ; FEATURE: US-09-302-812-38	
Ali Pre	Length: 2	
Sco	89.50 Matches: 5	
Bes Que DB:	cal Similarity: 20.38% Mismatches: atch: 5.05% Indels: 4 Gaps:	
us-	US-09-848-852A-3 (1-332) x US-09-302-812-38 (1-29793)	
δỳ	59 GluLysAlaGlyGlnHisSerProLeuArgGluGluHisValThrCy	le .78
g	Db 26932 GAAAAAGATCAAAATTAAAAATTAAAAGAAGAAGTTGAGAAATTA	TA 26885
ò	79 LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeu	al 98
qq	Db 26884 ATCGAIGAACAAGAAGAIGAATAATA	TA 26858
δy	66	114
g	Db 26857 CTAGCTGAAATGCAATTCGAAATTTTCCAAATAAAAGCAGAGACAGAAGCTAGAAGATTG	rg 26798
δy	Qy 115 LysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetVal	al 134
QQ	26797 AAGAAGTIGIT	26756
20	Ov 135 AraGlvDheAraValAlaTvrIvsAraHisValIenThrWetAspAspIen	151

ARG) REACT

Oy 59 GluLysAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIle 78	26932 GAAAAAGATCAAAAAAATTTAAAAGAAGAAGTTGAGAAATTA	Oy 79 LeubapoluPheLeuGlnThrTyrGlySerLeulleProLeuSerThrAspGluVal 98 :::	Qy 99GluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArg 114	Db 26857 CTAGCTGAAATGCAATTCGAAATTTCCAAATAAAAGCAGAGACAGAAGATTG 26798 Ov 115 LvsGlvLeuValLeuGlnLeuIleGlnSerTvrGlnArdMetProGlvAsnAlaMetVal 134	26797 AAGAAGTIGTIGATAATGAGAAATGAAGATTTCTCAATTCTC	135 ArgGlyPheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeu	DD 26/55AAAACTAAATATGAGGATCTTCAAAAACAATTTATGATTTGTCGCCATAT 26/U5  Qy 152GlyThrLeuTyrGlyGlnAsnTrpLeu 160	26704 CCGGTTAACGGTTACGGTGGAATATTAATTGGTGATGAAACACCGAAACAAGGAAGTTG	Qy 161 AsnaspGlnValMetAsnMetTyrGlyAspLeu 171	Qy         172ValMetAspThrValProGluLysValHisPhePheAsnSerPhePheTyrAsp 189           .:::::::::::   ::: :::  ::	190IysLeuArgThrLysGlyTyrAspGly	DD 26524 ATACTTATAACAAAAAAGATGGAAGACAACAACAACATCATCAAAAACTTGAAGACGAA 26465	Oy 199 ValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeulleProlle 218	219	Qy 238 TyrPheAsp-SerGlnArgThrLeuAsnArgArgCysProLysHisIleAlaLysTy 256 ::::    :::    ::::    ::::    ph 26344 mmmcCgaantcaacaaaaagaangaangaangaangaangaangaangaa	256 rLeuGlnAlaGluAlayaLysLysspargLeuAspPheHisGlnGlyTrpLysGlyTy 276 :::::::::::::::::::::::::::::::::::	276 rPheLysMetasn 280 ::::           26245 TIGGAACITCAAC 26233	ESULT 10 S-09-511- Sequence Patent N	GENERAL INFOR APPLICANT: APPLICANT: APPLICANT:	; APPLICANT: LIN, WINSTON ; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY(ADP-RIBOSE) GLYCOHYDROLASE (PARG) ; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREAC ; TITLE OF INVENTION: THEREWITH ; FILE REFERENCE: NIAD 201	; CURRENT APPLICATION NUMBER: US/09/511,507 ; CURRENT FILING DATE: 2000-02-23 ; PRIOR APPLICATION NUMBER: 09/302,812
Db 26755AAAACTAAATATGAGGATCTTCAAAAACAATTTATGTTGTCGCCATAT 26705	152GlnAsnTrpLeu	GGTGGAATATTAATTGGTGATGAAACACCGAAACAAGA AsnMetTyrGlyas	:::   Db 26644 ATGGATCAACTTTTGGACAAATTAAAAGTATTAAATGATGGAGATTATTATGACATTTTC 26585	OY 172ValMetAspThrValProGluLysValHisPheAbeAsnSerPhePheTyrAsp 189 ::::::::            Db 26584 CACTTGGTGGAAACTATTGACAAGATCATAGTCACGTTTTTTTT		26524 ATACTTATAACAAAAAAGATGGAAGACAACAAACAGATCATTCAAAAACTTGAAGACGAA	<pre>UY 199 VAILYSARGITFITATINELYSASDVAIASPILEFINGASDLLSGULGULGULGULGULGULGULGULGULGULGULGULGULG</pre>	219 HisLeuGluValHisTrpSerLeulleSerValAspValArgArgArgThrlleThr	Db 26404 GAAAACAAAGATGATTATCTCTTAGTGACAGTGGAATTCCAAAAAAGAATATTCTG 26345 Qy 238 TyrPheAsp-SerGlnArgThrLeuAsnArgArgCysProLysHislleAlaLysTy 256	Db 26344 TTTTCCGAACTCAAGAAAAGAATGAAGATTAAAATGCTTCAAGAATCCTTCAAGATT 26285 Ov 256 rIeuGlnAlaGluAlaValivsAsbaraTolenAspPheHisGlnGlvTrolysGlvTv 276	26284 TATCAGAAGGATAGTATGAAAAAGTCATGGAGAAATTT	Qy 276 rPheLysMetAsn 280	Db 26245 TTGGAACTTCAAC 26233 RESULT 9	-38/c , Applicatic 6337202 ORMATION:	<pre>// APPLICANT: JACOBSON, Myron K. // APPLICANT: JACOBSON, Blaine L. // APPLICANT: LIN, Winston // APPLICANT: LIN, Winston</pre>	AL POLY(ADP-RIBOSE) GLYCOHYDROL GMENTS THEREOF, AND ANTIBODIES	TION NU DATE: ON NUME TE: 19	SEQ ID NOS: 29793 A : Caenorhabadi	US-09-511-477-38 Alignment Scores:	d. No.: 33.3 re: 89.50 cent Similarity: 41.51% r Local Similarity: 20.38% ry Match: 5.05%	Gaps: 19-511-477-38 (1-29793)

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Db 26245 TTGGAACTTCAAC 26233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TyrPheAsp-SerGlnArgThrLeuAsnArg---ArgCysProLysHisIleAlaLysTy 256
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                                                                                                                                                                                                                                                                                                                     LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal
                                                                                                                                                                                                                                                                                                                                                                            -----GluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArg-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -------GlyThrLeuTyrGly-------GlnAsnTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                     29793
54
56
81
74
                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                   ORGANISM: Caenorhabaditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnAspGlnValMetAsnMet----
  1999-04-30
                                                                                                                                      33.3
89.50
41.51%
20.38%
5.05%
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PRIOR FILLING DATE: 19:
NUMBER OF SEQ ID NOS:
SEQ ID NO 38
LENGTH: 29793
                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                             US-09-511-507-38
                                                         TYPE: DNA
                                                                                   FEATURE
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RESULT 11
US-09-356-952-12
is Sequence 12, Application US/09356952
is Patent No. 611/663
is GENERAL INFORMATION
is APPLICANT: Boriack-Sjodin, Ann
is APPLICANT: Boriack-Sjodin, Ann
is APPLICANT: Boriack-Sjodin, Dafna
is APPLICANT: Boriack-Sjodin, Dafna
is APPLICANT: Cole, Philip
is APPLICANT: Kuriyan, John
if TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
if TITLE OF INVENTION: THEREOF
if TITLE OF INVENTION UNMER: US/09/356,952
if CURRENT APPLICATION NUMBER: US/09/356,952
if CURRENT FILING DATE: 1999-07-19
is EARLIER APPLICATION NUMBER: 60/093,631
is RARLIER PLING DATE: 1998-07-21
is NUMBER OF SEQ ID NOS: 14
is SOGTWARE: Patentin Ver: 2.0
is SEQ ID NO 32-36
is SEQ ID NO 32-36
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-------GTTATAGAAGAGATTTTAGAAATA 32408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrTyrGlySerLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIle 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 SerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGln
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Mismatches:
Indels:
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19.93%
4.99%
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Best Local Similarity:
Query Match:
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TYPE: DNA
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US-09-356-952-12
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Oy 204 LysasnValaspilePheasnLysGluLeuLeuLeulleProlleHisLeuGluValHis 223	Db 2806 CGTACTTTCAATGAAGAAGAACAAGTATATCATCTAAATGAACGG 2853
erGlnArg 243	Qy 191 LeuargThrLysGlyTyraspGlyValLysArgTrpThrLysAsn 205 
2097 INCHARGE SEASON AND STATE SEASON	<pre>Qy 206 ValAspilePheAsnLysGlu</pre>
2502 NOOMITTICSHARKAATAWAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Qy 220LeuGluValHisTrpSerLeuIleSerValAspValArgArgThrIleThr 237
284 GlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHisLeu 301	Qy 238 TyrpheAspSerGlnArgThrLeuAsnArgArgCysProLysHislleAlaLysTyrLeu 257 
302AlaLeuSerGInProPheSerPheThrGInGInAsp 313 33072 AAGITTTTCGCAATTAAACGGCGTCATTTCAACAACAGAG 3119	Qy 258 GlnalaGlualaValLysLysAspArgLeuAspPheHisGlnGly-TrpLysGl 275 
	<pre>Qy 275 yTyrPheLysMetAsnValAlaArg</pre>
Patent No. 6380370 GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al	Qy 290 sGlyAlaPheValLeuGlnTyrCysLys
	306 oPheSerPheThrGlnGlnAspWetProLysLeuArgArgGlnIle
CURRENT APPLICATION NUMBER: US/09/134,001C ; CORRENT FILING DATE: 1998-08-13	
FRIOR PELLING NUMBER: US 60/064,964  PRIOR PILING DATE: 1997-11-08  PRIOR APPLICATION NUMBER: US 60/055,779  PROPETING DATE: 1997-08-14  NUMBER OF SEQ ID NOS: 5674  SEQ ID NO 405	
aphyl 05	; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC ;; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS ;; FILE REFERENCE: GTC-007 ; CURRENT APPLICATION NUMBER: US/09/134,0010
Alignment Scores:  Pred. No.: Score: 87.50 Matches: 60 Percent Similarity: 43.36% Conservative: 51 Best Local Similarity: 23.44% Mismatches: 96 Ouery Match: 4.94% Indels: 50 DB:	CURRENT FILING DATE: 1998-08-13  PRIOR APPLICATION NUMBER: US 60/064,964  PRIOR FILING DATE: 1997-11-08  PRIOR PLING DATE: 1997-10-08  PRIOR FILING DATE: 1997-08-14  NUMBER OF SEQ ID NOS: 5674  EMORTH: 2184
US-09-848-852A-3 (1-332) x US-09-134-001C-405 (1-3456)	; TYPE: DNA ; ORGANISM: Staphylococcus epidermidis
Qy 98 ValGluLysLeuGluAspilePheGlnGlnGluPheSerThrProSerArgLysGlyLeu 117 ::: ::    :::	134 -UULC-123U ent Scores: 1.47 Length: 2
Oy 118 ValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArg 135 	ore:  86.00 Matches: rcent Similarity: 36.26% Conservative: st Local Similarity: 18.70% Mismatches: ery Match: 4.85% Indels:
Qy 136 GlyPhe	DB: US-09-848-852A-3 (1-332) x US-09-134-001C-1230 (1-2184)
MetAsnMetTyrGlyAsp	<pre>Qy 69 GluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGlnThrTyrGly 87</pre>
171	Qy 88 SerLeulleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGln 107 :::

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132	127	147	167 273	187	207	399	247	265	285	301	603	320	650		
Db 118 TTGATTATTCTGAAT	Oy 108 GluPheSerThrProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArg :::	Oy 128 MetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLySArgHisValLeuThr	MetaspaspleuGlyThrLeuTyrGlyGlnasnTrpLe ::::::	OY 168 TYTG1YASPLeuValMetAspThrValProGluLysValHisPhePheAsnSerPhePhe	Oy 188 TyraspLysLeuargThrLysGlyTyraspGlyValLysargTrpThrLysasnValasp   ::      Db 331 TTAGAAAAGTTTAAT	Oy 208 IlePheAsnLysGluLeuLeuLleProlleHisLeuGluValHisTrpSerLeulle	Qy 228 SerValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArg	Oy 248 ArgCysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAsp	Oy 266 ArgLeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsn Db 520 CATATTCGATTTAATGAAATTTTAAAAAATTTAAAAAATTTAAAAAA	286	Db 562TCATTTGTTCTAAATATGAAGTATGTAAATAAGTTTGTA	Oy 302AlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGln :::	321 IleTyr 322	Db 640 GTCTAT 645	RESULT 14 US-08-531-927B-8 Sequence 8, Application US/08531927B Fatent No. 5840491 TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph Patent No. 5840491 TITLE OF INVENTION: Disease Gene and Uses Thereof NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STREET: Wasacchusetts COUNTRY: USA ZIF: OA273-4799 KEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC COMPATIBLE COMPUTER: LBM PC COMPATIBLE COMPUTER: LBM PC COMPATIBLE SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN PC-DOS/MS-DOS SOFTWARE: PATENTIN DATA:
П	<b>о</b> д	σд	G D	0 0	5 4	5 1	3 4	<b>υ</b> Δ	3 4	J	ı	J 2	. 0	Ц	MD CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 uPheSerThr-------ProSerArgLys--------115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 TTATAAGGAACACTGGTTTACAGTTAGAAATTA-------GGAAAACAGTGGTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 uAspGluPheLeuGln---ThrTyrGlySerLeuIleProLeuSerThrAspGluValVa 98
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223 TTATCGCACGTGTGACAGCAGCCTTCTGGAAATATGGATGACAGTGGTTTTTTCTCTAT
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 12-SEP-1994
ATTORNEY, AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: ATH95-01A
FELECOMMUNICATION INFORMATION:
TELEPAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-902-622-1
; Sequence 1, Application US/08902632
; General No. 6008025
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                0.672
84.00
38.98%
25.42%
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Best Local Similarity:
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us-09-848-852a-3.rni

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---CTAGCGGAGAACAAGAGGATTCCC----- 3791
                                                                                            APPLICANT: TAKAGI, Masahiro
APPLICANT: IMANAKA, Tadayuki
TITLE OF INVENTION: Modified Thermostable DNA Polymerase,
TITLE OF INVENTION: and DNA Polymerase Composition for Nucleic Acid
TITLE OF INVENTION: Amplification
CORRESPONDENCE ADDRESS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AlaSerIle-----LeuIleSerAsnValCysSerIleGlyAspHisValAlaGln 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHisLeuAlaProProAsp 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 GluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLys 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3726 AAGAAGATCGGCTACCTGCTCTTTGAGAACATGTGCGGTGTC-------
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch floppy disk, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: hyperthermophilic archaeon STRAIN: KOD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE: CUICALTEIL CITASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 198911/96
FILING DATE: 99-JUL-1996
APPLICATION NUMBER: JP 200446/96
APPLICATION NUMBER: JP 20046/96
APPLICATION NUMBER: JP 20046/96
ATTORNEY/AGENT INFORMATION:
NAME: GREASON, Edward W.
REGISTRATION NUMBER: 18,918
REFERENCE/DOCKET NUMBER: 2418/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425/7200
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,632
FILING DATE: CONCURRENT HEREWITH
KOMATSUBARA, Hideyuki
                                                            KAWAKAMI, Bunsei
KAWAMURA, Yoshihisa
                                                                                                                                                                                                                                           ADDRESSEE: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 5342 base pairs
                                      KAMIMURA, Hideki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
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31.90%
17.86%
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EDNESS: double
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Best Local Similarity:
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STRANDEDNESS:
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Pred. No.:
                                                                             APPLICANT:
APPLICANT:
APPLICANT:
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1038 GCCTACTCCACACGTGATCCCCAACGAAGTCCTGAGCGAGGTCTTTG 4097
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| 1200 GTGCTCGACCGCGTTGATGTGGAAGACTACGATGGTTATGTCTATGACCTG 4259
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                                                                                                                                                                                               81 GluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValValGluLys 100
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61 AlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAsp 80
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O9vpiO drosophila
O9vwk5 drosophila
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Ottenwealder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.; Tampe J., Heubner D., Mambutt R., Korn B., Klein M., Poustka A.; Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).

BEBL: ALGOSQB3; CAB43384.1; --
HSSP; O02724; IEUV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 42.2 kDa protein.
0KF2DF586K0919.
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Q8RWN0
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09P6U5
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Q23238
               Q9VWK5
Q9FP66
Q9WV12
                                                              Q9M908
Q94F30
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Q8TBY4
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09LSS7
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                                                                                              095KG4
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MEDLINE=21154917; PubMed=11230166;
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SEQUENCE FROM N.A.
NCBI_TaxID=9606;
311
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88.726 Million cell updates/sec
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                                                                                                          December 16, 2002, 19:34:35; Search time 771 Seconds
                              Compugen Ltd
               GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compu
                                                                                                                                                                                                                                                                                                                        of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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Maximum DB seq length: 200000000
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Gaps .. O Length 371; 0; Indels l protein. 371 AA; 42234 MW; EEE87C5885CA5082 CRC64; cch 94.1%; Score 1667; DB 4; L al Similarity 100.0%; Pred. No. 1.7e-136; 314; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches

InterPro; IPR003653; SUMO protease. Pfam; PF02902; Peptidase\_C48; 1. Hypothetical protein.

homo sapien
7 mus musculu
homo sapien
macaca fasc

Q9ep97 mus Q96hi0 homo

homo sapien

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Q8wp32 1 Q96sa5 1 Q9nwf3 1 Q9p0u3 1 Q9p215 1

Q96H10 Q8WP32 Q96SA5 Q9NWF3 Q9P0U3 Q96SR2 Q96SR2 Q9HC62

994.1 997.1

1667 1667 1667 168.5 788.5 788.5 490 456 393 393 387.5 385.5

755 446 191 643

sapien sapien

homo

09y3w9 09h414 096ps4

Description

homo

Q9H4L4 Q96PS4 Q9EP97

Q9Y3W9

Match Length DB

Query

Result Ş. SEQUENCE

sapien sapien sapien sapien

homo

homod Q9cum5 mus

**09hc62** 

LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78 13

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Q91zx6 mus musculu Q9d4z0 mus musculu Q9eqe1 rattus norv

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LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117
                                                     VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ 258
                                                                                                                                                                                                                                                                 259 AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                                                                                                                         LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.1%; Score 1667; DB 4; L
100.0%; Pred. No. 3.2e-136;
Live 0; Mismatches 0;
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MEDLINE-20267842; PubMed-10806345;
Yeh E.T., Gong D., Kamitani T.;
"Ubiquitin-like proteins: new wines in IGene 248:1-14(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
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SENP3.
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EMBL; AY008763; AAG33252.1;
HSSP; Q02724; IEUV.
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                                                                                                                                                                                                                                                                                                                                             RQIYKELCHCKLTV 332
                                                                                                                                                                                                                                                                                                                                                                 Similarity
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01-JUN-2002
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Matches 314;
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LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_raxID-10090;
                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
Choi S.J., Jeon Y.J., Kim K.I., Nishimori S., Suzuki T., Uchida Shimbara N., Tanaka K., Chung C.H.;
Shimbara N., Tanaka K., Chung C.H.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF199459; AAL25652.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574 AA; 65009 MW; E495137EE7500741 CRC64;
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, E
Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Sentrin/SUMO-specific protease (SMT3 isopeptidase 1)
SMT31P1 OR SENP3 OR SMT31P.
                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1667; DB 4; 1
Pred. No. 3.2e-136;
                                                                                                                                                                                                               sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.1%; Sco. 100.0%; Pred. No. 0. 0. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                         Created)
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Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                               PRT;
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                                                                                                                                                                                                               Last
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                                                                                                                                                 PRELIMINARY;
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                   ROIYKELCHCKLTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
RQIYKELCHCKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 314; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C48.003;
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Pfam; PF02902; Peptidase_C48; 1.
                                                   Best Local Similarity
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                     SEQUENCE
                                         Query Match
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                                                                                      PubMed=11029585;
Nishida T., Tanaka H., Yasuda H.;
Nishida T., Tanaka H., Yasuda H.;
A novel mammalian Smt3-specific isopeptidase 1 (SMT3IP1) localized in the nucleolus at interphase.";
Eur. J. Biochem. 267:6423-6427(2000).
EMBL; AXO08764; AAG38253.1; -.
HSSP; Q02724; IEUV.
                                                                                                                                                                                                                                                                                                  LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
                                                                                                                                                                                                                                                                                                                                          VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
                                                                                                                                                                                                                                                                                                                                                                                 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                      LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                              VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MXT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0008589; AAH08589.1; -.
MEROPS; C48.008; -.
                                                                                                                                                                                                                          568 AA; 6403 MW; 655F1FAB1AB62EA8 CRC64;
                                      Yeh E.T., Gong L., Kamitani T.;
"Ubiquitin-like proteins: new wines in new bottles.";
Gene 248:1-14(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unknown (Protein for IMAGE:3448367) (Fragment).
                                                                                                                                                                                                                                               98.1%; Score 1637; DB 11; 98.1%; Pred. No. 1.3e-133;
                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                      MEROPS; C48 003; --
MGD; MGI:2158736; Smt3ipl.
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003653; SUMO_protease
                   STRAIN=C57BL/6J;
MEDLINE=20267842; PubMed=10806345;
                                                                                                                                                                                                                                                                  Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQIYKELCHCKLTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
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                                                                                                                                                                                                                 Protease.
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                                                                                                                                                                                       117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                              PEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFYDSQGIHFKFCVENIRKYLLTEAREKNRPEFLQGWQTAVTKCIPQQKNDSDCGVFVLQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 QEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMAEEAERPGEKAGQH-SPLREEHVT-CVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQ 106
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                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=TESTIS;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
Terao K., Sugano S.;
"Isolation of novel full-length cDNA clones from macaque testis cDNA
libraries.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQ
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 86.3 kba protein.
Hypothetical 86.3 kba protein.
Hypothetical Secicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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                                               Length 537;
                                                                                                         ee; Indels
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EMBL; AB074(NY 1291)

InterPro; IPR003653; SUMO_protease.

Pfam; PF02902; Peptidase_C48; 1.

Hypothetical protein.

SEQUENCE 755 AA; 86290 MW; 40EC773CA29B8CEA CRC64;
537 AA; 61769 MW; 18F609C41D4B7DF9 CRC64;
                                                  44.5%; Score 789; DB 4; 54.0%; Pred. No. 5.1e-60; ive 54; Mismatches 66
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Best Local Similarity 53.5%
Matches 152; Conservative
                                                                                                         Matches 148; Conservative
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TISSUE-EMBRYO;
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351 SFYDSQGIHFKFCVENIRKYLLIEAREKNRPEFLQGWQTAVTKCIPQQKNDSDCGVFVLQ 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 TYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GKNSQKASPVDDEQLSVCLSGFLDEVMKKYGSLVPLSEKEVLGRLKDVFNEDFC--NRKP 233
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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9
                                                                                                                                                                                                                                                                                                                                                                     Length 446;
                                                                                                                                                                                                                                                                                                                                                                                         67; Indels
                                                                                                                                                                                                                                                                                 Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                               446 AA; 50902 MW; 3810DCC23655D646 CRC64;
                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 20.5 kDa protein.
                                                                                                                                                                                                                                                  Wang Y.-G., Li T.; "Identification of FKSG45, a novel gene located
                                                                                                                                                                                                                                                                                                                                                                   Query Match
44.2%; Score 784; DB 4;
Best Local Similarity 53.6%; Pred. No. 1.1e-59;
Matches 147; Conservative 54; Mismatches 67;
                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 YCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446
                                                                                                                                                                                                                                                                                                              InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
Protease.
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                                                                                                                                                              Sumo/sentrin-specific protease.
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MEROPS; C48.008; -.
                                                                                                          PRELIMINARY;
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01-JUN-2002
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                                                                                                                                                                          FKSG45
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                                                                                     RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                493
                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 EE-HVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 MPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a Novel Sentrin-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AKO00923; BAA914881; --
SEQUENCE 191 AA; 20457 MW; B9F2B6F629F31612 CRC64;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20119292; PubMed=10652325;
Gong L., Millas S., Maul G.G., Yeh B.T.H.;
"Differential Regulation of Sentrinized Proteins by
specific Protease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Sentrin/SUMO-specific protease.
                                                                                                                                                                                                                                                                                  27.7%; Score 490; DB 4; L
100.0%; Pred. No. 1.1e-34;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643
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EMBL; AF149770; AAF31171.1; -.
HSSP; Q02724; 1EUV.
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Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE=PLACENTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 TLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGYFKMN-VARQNNDSDCGAFVLQYCKHL 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:65-73 (2000).
EMBL; AB037752; BAA92569.1; -.
HSSP; Q02724; IEUV.
                            : : : | | | | | | : : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 412;
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Local Similarity 29.6%; Pred. No. 8.5e-26;
nes 97; Conservative 64; Mismatches 107; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pfam; PF02902; Peptidase_C48; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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Matches
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y., Matkaunawa H., Ishii S., Kawai Y., Sato K., Yamamoto J., Wakamatsu A., Nagahari K., Masuho Y., Sasaki N.; "NEDO human CDNA sequencing project."; Sasaki N.; EMBL, ARVD7599; BAB55222.1; -. MEROPS; C48.007; -. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 SRRGYQLEP-----GENGLERK-- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 --VSIIETKEKNCSGKERDRRTDDLLELTEDM-EKEISNALGHGPODEILSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRR
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Catarrhini; Hominidae; Homo.
                                                                                                                                     Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 589;
                                                                                            Homo sapiens (Human).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
MCBI_TaxID=9606;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI51697; AAG15309.2; -.
HSSP; 002124; 1EUV.
MEROPS; C48.007; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
SEQUENCE 589 AA; 67890 MW; 75836FC41672E436 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DUN-2002 (TrEMBLrel. 21, Last annotation update) CDNA FLJ14693 fis, clone NT2RP2005360, weakly similar saplens sentrin/SUMO-specific protease (SENPI) mRNA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%; Score 393; DB 4; I
29.6%; Pred. No. 1.4e-25;
iive 64; Mismatches 107;
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561 RDKPITFTQHQMPLFRKKMVWEILHQQL 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 LSQPFSFTQQDMPKLRRQIYKELCHCKL 330
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 16, (TrEMBLrel. 16, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sentrin-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 29.6 ses 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeh E.T.H.;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09HC62;
01-MAR-2001 (
01-MAR-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches
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01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last seq 01-JUN-2002 (TrEMBLrel. 21, Last ann SUMO-1/SML5-specific isopeptidase 2. 4930538C18RIK OR SMT31P2.

Mus musculus (Mouse)
                     MGD; MGI:2149738; 4930444620Rik.
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003653; SUMO protease.
Pfam; PF02902; Peptidase_048; 1.
SEQUENCE 541 AA; 62227 MW; 84AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1923076; 4930538C18Rik.
                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                       NON_TER 1
SEQUENCE 357 AA;
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ses 93; Conserv
     MEROPS; C48.010; -
                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                  Query Fig. Best Local Similar
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Matches
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T.,
Ruchl P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J.,
Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ashrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Askai K., Okido T., Furuno M., Anne D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248
                                                                                                                                                                                                                                                                                                                                  73 TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                          188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               561
                                                                                                                                                                                                                                                                               SRRGYQLEP------DLSEEVSARLRLGS--------GSNGLLRRK-- 343
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                               13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 ICEILLQYLQDESKTKRNSDLNLLEWTHHSMKPH---EIPQQLNGSDCGMFTCKYADYIS
                                                                                                                                                                                                                                                                                                                                                                    | | :: | | :: | | :: | | 344 --VSIIETKEKNCSGKERDRRTDDLLEL/TEDM-EKEISNALGHGPQDEILSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                               60;
                                                                                                                               Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Adult male testis CDNA, RIKEN full-length enriched library,
clone:4930444620, full insert sequence (Fragment).
                                                                                                                          22.2%; Score 393; DB 4; Length 59(29.6%; Pred. No. 1.4e-25;
ive 64; Mismatches 107; Indels
                                                                          444EDE041E96561F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               562 RDKPITFTQHQMPLFRKKMVWEILHQQL 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEÓDENCE FROM N.A.
STRÁIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSQPFSFTQQDMPKLRRQIYKELCHCKL
                                                                          67952 MW;
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EMBL; AK015380; BAB29820.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                     1 Similarity 29.6 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                          590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4930444G20RIK.
                                                                                                                          Query Match
Best Local
                                                     Protease
                                                                          SEQUENCE
                                                                                                                             Match
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                                                                                                                                                                               Matches
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  SWBB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 LE----WKQYSVTSEEIPLQLNGSDCGMFTCKYADYIARDQPVTFSQQHMPTFRKRWVWE 350
                                                                                                                                                                                             49 GMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQE 108
                                                                                                                                                                                                                                                                                                                     109 FSTPSRKG----LVLQLIQSYQRMPGNAMVRG-----PRVAYKRHVLTMDDLGTLY 155
                                                                                                                                                                                                                                                                                                                                                             55 ERPGEKAGQHSPLREEHVTC---VQSILDEFLQTYGSLIPLS----TDEVVEKLEDIFQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 QEFSTPSRKGLVLQLIQSYQRMPGNAMVRG-----FRVAYKRHVLTMDDLGTLYGQNWLN 161
                                                                                                                                                                                                                                  | : | : | : | : | : | 82 GNSLEPDLPGTQA------QIILDS--GKGNSLFPNKVAVLAAEKKPI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 NGQWLNDEVINFYMNLLVERNENQGYPALHVFSTFFFYPKLKHGGYSSVKRWTRGINLFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEA----VKKDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDFHQGWKGY -- FKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                156 GQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=21486428; PubMed=11489887;
Nishida T., Kaneko F., Kitagawa M., Yasuda H.;
Nishida T., Kaneko F., Kitagawa M., Yasuda H.;
Characterization of a Novel Mammalian SUMO-1/Smt3-specific
Isopeptidase, a Homologue of Rat Axam, Which Is an Axin-binding
Protein Promoting beta-Catenin Degradation.";
J. Blol. Chem. 276:39060-39066(2001).

EMBL. AF368904; AAL14437.1;
MEROPS; C48.007;
                                                           21.9%; Score 387.5; DB 11; Length 357; 32.0%; Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; Length 541;
41001 MW; 9453B4A1989BD3BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84AAOBB6CB7E00CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                               Score 38/.2,
Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.8%; Score 385.5; DB 11;
31.4%; Pred. No. 5.6e-25;
ive 62; Mismatches 106;
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Rawai J., Shinagawa A., Shibata X.,
Rawai J., Shinagawa A., Shibata X., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rabischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Buta J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Ra Brownstein M.J., Hull D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Rasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Rayashizaki W., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Rasaki Y., Kawashi Y., Kawaji H., Kohtsuki S.,
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217
                                                                                                                                                       218 IHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGY 276
                                                                                                                                                                                                                                                                                                                                         484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 QEFSTPSRKGLVLQLIQSYQRMPGNAMVRG-----FRVAYKRHVLTMDDLGTLYGQNWLN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 EKEGTRGHOMEPDLSEEVSARLRLGSGSNGLLRRKISVLEIKEKNFPSKEKDRRTEDLF- 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Gaps
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                DQVMNMYGDLVMDTVPEK----VHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIP
                                                                                                                                                                                                                                                                                                                                                                                                               277 FKM--NVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 SMKPHEIPQQLNGSDCGMFTCKYADYISRDKPITFTQHQMPLFRKKMVWEILHQQL 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.8%; Score 385.5; DB 11; Length 588; 31.4%; Pred. No. 6.4e-25; ive 62; Mismatches 106; Indels 35;
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Interpro; IPRO03653; SUMO_protease.
Pfan; PF02902; Peptidase_C48; 1.
SEQUENCE 588 AA; 67579 MW; 09B56796CA194847 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  588 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK015987; BAB30067.1; -.
HSSP; Q02724; 1EUV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4930538C18Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
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Q9D4Z0
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Search completed: December 16, 2002, 20:11:15 Job time: 773 secs

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us-09-848-852a-3.rapb

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2002, 19:26:20 ; Search time 167 Seconds Run on:

(without alignments)
33.125 Million cell updates/sec

US-09-848-852A-3

1772 1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105981 seqs, 16662342 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Published\_Applications\_AA:\*

Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.:\* /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	moradi rasar	Sequence 3, Appli		7	Sequence 13640, A	Sequence 13443, A	Sequence 34, Appl	Sequence 614, App	Sequence 200, App	Sequence 394, App	Sequence 16, Appl	Sequence 11364, A	Sequence 5222, Ap	Sequence 12143, A	Sequence 16, Appl	Sequence 46, Appl	Sequence 46, Appl	Sequence 15, Appl	Sequence 35, Appl	
£		US-09-848-852A-3	US-09-856-247A-2	US-10-008-461-2	US-09-815-242-13640	US-09-815-242-13443	US-09-866-582-34	US-09-925-302-614	US-09-765-272-200	US-09-801-368-394	US-09-890-813-16	US-09-815-242-11364	US-09-815-242-5222	US-09-815-242-12143	US-10-041-007-16	US-09-887-586A-46	US-09-903-012-46	US-10-041-007-15	US-09-866-582-35	US-10-007-706-1
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% Query Match Length DR		332	621	212	427	427	824	304	674	803	439	865	638	642	782	782	782	817	820	1503
& Query Match		100.0	12.6	6.9	5.1	5.1	4.9	4.7	4.7	4.6	4.5	4.5	4.5	4.5	4 . 4	4.4	4.4	4.4	4.4	4.4
Score	1	1772	222.5	122.5	90.5	89.5	98	84	82.5	82	80	80	79	79	78.5	78.5	78.5	78.5	78.5	78.5
Result	: :	Н	7	æ	7	2	9	. 7	<b>&amp;</b>	6	10	11	12	13	14	15	16	17	18	19

LENGTH: 332 amino acids TYPE: amino acid

SEQUENCE CHARACTERISTICS

Sequence 27, Appl Sequence 1086, A Sequence 11557, A Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 2126, Appl Sequence 1152, A Sequence 1152, A Sequence 2, Appl Sequence 2, Appl Sequence 50, Appl Sequence 50, Appl Sequence 52, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 11036, A Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 1136, A Sequence 21, Appl Sequence 21, Appl	•
US-09-905-173-27 US-09-815-247-4912 US-09-815-242-10686 US-09-815-242-11557 US-09-807-586A-24 US-09-807-586A-24 US-09-807-586A-24 US-09-815-242-5126 US-09-815-242-11522 US-09-819-249-2 US-09-919-445-50 US-09-919-446-50 US-09-917-486-52 US-09-938-956-7 US-09-903-012-52 US-09-903-012-52 US-09-903-012-52 US-09-903-012-52 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036 US-09-815-242-11036	
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8 5 7 7 7 7 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9	
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Tang, Y. Tom
Corley, Neil C.
Guegler, Karl J.
Yue, Henry
Patterson, Chandra
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/848,852A
FILING DATE: 07-May-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0515 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 09/069,725
FILING DATE: <Unknown>
                                           Sequence 3, Application US/09848852A Patent No. US20020106373A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: USA
ZIP: 94304
RESULT 1
US-09-848-852A-3
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us-09-848-852a-3.rapb

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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      APPLICANT: Barbara Ink
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Best Local Similarity
Matches 47; Conserv
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612 AHLILT 617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09856247A
Patent NO. US20020151028A1
GENERAL INFORMATION:
APPLICANT: Lima, Christopher
APPLICANT: Lima, Christopher
APPLICANT: Lima, Sessesova, Elena
TITLE OF INVENTION: Structure-Based Drug Design for Ulp1 Protease Substrates
FILE REPERBNCE: 2650/1681-US1
CURRENT APPLICATION NUMBER: US/09/856,247A
CURRENT FILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-05-18
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                                                                                                                                                                                                                                                                                                  61 AGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                        61 AGGHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQOEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                       SQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKH 300
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                                                                                                                                                   Gaps
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                                                                                                                                                                                               1 MYSAQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEK
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0
                                                                                                                      Length 332;
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                                                                                                                                                  Indels
                                                                                                                   Query Match 100.0%; Score 1772; DB 10; Best Local Similarity 100.0%; Pred. No. 3.6e-167; Matches 332; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,5e-14;
nes 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LALSQPFSFTQQDMPKLRRQIYKELCHCKLTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-848-852A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
                                          LIBRARY: BEPINOT01
CLONE: 2056178
               TOPOLOGY: 11
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-856-247A-2
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-- QRTLNRRCPKHIAKYLQAEAVKKD
                           56 PEVIQFIKCISNPAEIAMFLEPLDLPNKRVVFLAINDNSNQAAGGTHWSLLVYLQDKNSF
                                                                                             RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.9%; Score 122.5; DB 12;
23.9%; Pred. No. 0.0001;
tive 32; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alan Lewis
TITLE OF INVENTION: New Protein
FILE REFERENCE: QG1034 (p8020)
CURRENT APPLICATION NUMBER: US/10/008,461
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242
  KELLLIPIHL - EVHWSLISVDVRRRTITYFDS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13640, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                        US-10-008-461-2; Sequence 2, Application US/10008461; Patent No. US20020127692A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --CNTEALCONF-FROO 182
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12;

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82 FLQTYGSLIPLSTDEVVEKLEDIFQ-----QEFSTPSRKGLVLQLIQSYQRM-----P 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GNAM-VRGFRV-----AYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDT-----V 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 RMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGD--LVMDTVPEKVHFFN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 PEKVHFFNSFFYDK----LRTKGYDGVKRWTKNVDIFNKELLLIPIHL--EVHWSLISVD
                                                                                                                                                                                                                                                                                                                                                                                              Length 427;
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                                                                                                                                                                                                                                                                                                                                                                                        5.1%; Score 89.5; DB 10;
20.5%; Pred. No. 0.51;
tive 52; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 VRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLD 268
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APPLICANT: Pazour, Gregory J.
APPLICANT: Rosenbaum, Joei L.
APPLICANT: Rosenbaum, Joei L.
APPLICANT: Cole, Douglas G.
TITLE OF INVENTION: INTRAFLAGELLAR TRANSPORT: FILE REFERENCE: 07917-145001
CURRENT APPLICATION NUMBER: US/09/866,582
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,923
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%; Score 86; DB J
17.6%; Pred. No. 2.9;
tive 48; Mismatches
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34, Application US/09866582
Patent No. US20020127620A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus pneumoniae US-09-815-242-13443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.9%
Best Local Similarity 17.6%
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 57; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 PDSCLFFSTLAN------LYPGTPLAT------DIVGSEESISQINLTNLQENFTK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 KLAIGVRGKREVSEADCYRHHILLKLLFAMMFG--WTSDRFQKCYESGKIDASLSLEVEV 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 PDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Obligation, Kari L.
APPLICANT: Apskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tranick, John D.
APPLICANT: Tranick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: An Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
FILE REPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 VRRRIITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLD 268
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PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASSEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13640
     2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-815-242-13443
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RESULT 8
US-09-765-272-200
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (229)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                               241
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                                                                                           242 QRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHL 301
                                                                                                                           ---ECLRFLVRLCTDL 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 RDNYTCPTEEEXKAMVLQKTGGLFGLAVGLMQLFSDYKEDLKPLLNTLGLFFQIRDDYAN 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 MDTVPEKVHFFNSFFY---DKLRTKGY-DGVKRWTKNVDIFNKELLLIPIH----LEVHW 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 SFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITY---FDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 114;
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: Pal04
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PAtentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 84; DB 10; Length 304; 18.7%; Pred. No. 1.1;
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                                                                                                                                                           302 ALSQPFSFTQ----QDMPKLRQIYK 323
                                                                                                                                                                             -LALSQPFSFTQQDMPKLRRQIYKEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 YLEDVGSFEYTRNTLKELEAKAYKQI 279
                                                                                                                                                                                                                                                                       Sequence 614, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YQRMPGNAMV-----
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                                                                                                                        677 YKDTHRKFPENV
581 VIPTDPQV
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NAME/KEY: SITE
                                                                                                                                                                                                                                                        US-09-925-302-614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-925-302-614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                    APPLICANT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EKLED---IFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 ESEGMFYFHILGDSYYEKVYDNVŚIFENLYET------QEMKSFALISAWGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AYKRHVLTM--DDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150 LYKARLFEQLRFDIGKLGEDGYLNQKVY-----LLSEKVIYLNKSLYAYRIRKG-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 GVKR-WTKN-----VDIFNKELLLI-----PI--HLEVHWSLISVDVRR------RTIT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 EAERPGEKAGQHSPLRE---EHVTCVQS---ILDEFLQT-YGSLIPLSTDEVV---
                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERALIG SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.7%; Score 82.5; DB 10; 22.1%; Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                       Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/765,272
FILLING DATE: 22-0an-2001
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 08/961,083
FILLING DATE: «Unknown>
FILLING DATE: «Unknown>
APPLICATION NUMBER: NOW-961,083
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 200:
US-09-765-272-200
                                                                                                                                                                                        STREET: 9410 Key West Avenue
Sequence 200, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 394, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 674 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 200 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56; Conservative
                                                                                                                                                                                                                   CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 YFD---SQRTLNR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKEFEMKORLLNQ 271
                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-801-368-394
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Best Local
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18;

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309 LTLDPSKLWSR--ELIQQELDHVVEELEKIAVVHLLQHRSIISLIGNVQRSSLIL---EK 363
                                                                                                                                                                                                                                                                                                                                                                       94 TDEVVEKL---EDIFQQEFSTPSRK-GLVLQLIQSYQR-MPGNAM--VRGFR-----VA 140
                                                                                                                                                                                                                                                                                                                                                                                                                  141 YKRHVLTMDDLGT-LYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTK---- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 -GYDGVKRWTKNVDIFNKEL-----LLIPIHLEVHWSLISV--DVRRRTITYFDSQR 243
                                                                                                                                                                                                                                                                                             157 GSDL----TATTIGKALG----LREIQVWKDVDGVLTCDPNI-----YANAVPVPYLT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 KAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLS----TDEVVEKLEDIFQQEFSTPSR 114
                                                                                                                                                                                                                       45 GSDLGMAEEAERPGEKAGQHSPLREEHV----TCVQSILDEFLQTYGSLIP---LS 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 LKSNITMLDIVSTRMLGQYGFLAKVFSIFEDLGISV-------DSVATSEVSIS
                                                                                                                                                88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Oblise, Kari L.
APPLICANT: Oblisen, Kari L.
APPLICANT: Gyskind, Judith W.
APPLICANT: Eyskind, Judith W.
APPLICANT: Trawl, Daniel
APPLICANT: Trawl, John D.
APPLICANT: Trawl, John D.
APPLICANT: Trawl, John D.
APPLICANT: Trawl, John D.
APPLICANT: Xu, Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: 1000-11.A
CURRENT APPLICANTON NUMBER: 06/019, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253, 625
PRIOR PRILCATION NUMBER: 60/253, 938
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253, 308
PRIOR PILING DATE: 2000-12-22
PRIOR PRILCATION NUMBER: 60/269, 308
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
                                                                  4.5%; Score 80; DB 9; Length 439; 21.0%; Pred. No. 4.6; cive 52; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ;; ;; | |; | ||; | ||; | ||; | ||; | ||; | ||; | ||; | ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; ||; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 TLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSD 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
4.5%; Score 80; DB
Best Local Similarity 23.7%; Pred. No. 12;
Matches 36; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11364, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                Conservative
                                                                                                         Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
US-09-815-242-11364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Helico
US-09-815-242-11364
US-09-890-813-16
                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sllva, Jeff
APPLICANT: Sllva, Jeff
APPLICANT: Summers, Eiff
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 00/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin Version 3.0
SEQ ID NO 394
LENGTH: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 MVSKGDYDGQKNGKAKKIRSQLLKNPPETTSLINDVQNLLNSISKDYEN----ETVQXNE 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| :: :|| :: | :: | :: | SKLLEAESKEQIMEQIRNQLPAEKIQSMLPPTVLLKARINAY------KRNDKHLTNV 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDT-VPEKVHFFNSFFYDKLRTKGYDGVKRW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 TKNVDIFNKELLLIPIHLEVHWSLI-----SVDVRRRTITYFDSQRTLNRRCPKHIAKY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLEDIF-----QQEFSTPSRKGL--VLQLIQSYQRMPGNAM------VRGFRVAYKR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               644 LGIIADESS---GIDWDSSE-----YDADEPFKVEFLSDFLEDKLQ-KNYEG--DI 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 MAEEAERPGEKAGQHSPLREE------HVTCVQSILDEFLQTYGSLIPLSTDEVVE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.6%; Score 82; DB 10; Length 803; Best Local Similarity 22.2%; Pred. No. 6.8; Matches 56; Conservative 41; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09890813
Publication No. US20020183486A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: Aspartate Kinase
FILE REFERENCE: BB1430 PCT
CURRENT APPLICATION NUMBER: US/09/890,813
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/172944
PRIOR APPLICATION NUMBER: 60/172944
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Mccrosoft Office 97
SEQ ID NO 16
LENGTH: 439
                                                                                                                                                                                                                                                                                     No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Triticum aestivum
                           APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                       Maxon, Mary
Milne, Todd
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18.7%; Pred. No. 9.9;
tive 49; Mismatches
                                                                             US-09-815-242-12143;
; Sequence 12143, Application US/09815242
; Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-041-007-16
; Sequence 16, Application US/10041007
; Patent No. US30020164736A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 18.79
Matches 56; Conservative
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                                                             653 KAFDHQNLSEEELLGLKNILKEDFNAHVSLEDLKKASPIENFVAEKLKSDYENK----- 706
                                        115 KGLVLQLIQSYQRMPGNAMVRGFRVAY-----KRHVLTMDDLGT---LYGQNWLNDQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 VLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMD-----DLGTLYGQNWLNDQVMNMYGDL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EPDLLLLDEPTNHLDLET---TKWLEDYLRYFKGAI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 VMDTVPEKVHFFNSFFYDKLRTKGYD----GVKRWTKNVDIFNKELLLIPIHLEVHWSLI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RTLNRRCPKHIAKYLQAEAVKKDRLD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: PROKATYOTES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR PRICATION NUMBER: 60/205,78
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 4.5%; Score 79; DB 1 Local Similarity 18.7%; Pred. No. 9.8; es 56; Conservative 49; Mismatches
                                                                                                                    164 V-----MNMYGDLVMDTVPEKVHFFNSFFYD 189
                                                                                                                                               NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5222
LENGTH: 638
                                                                                                                                                                                                                                                         Sequence 5222, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                  APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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US-09-815-242-5222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 TYKTHMSRYESLSNQFEQLEGYQYESKIKTVLHGL-NFSEEDFNKPINDFSGGQKTRLSL 177
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APPLICANT: Zysklnd, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tramicto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-36
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-110-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILNG DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILNG DATE: 2000-12-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 12143
LENGTH: 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 ELKLFTEAVRWDLSFTENLPDYMKLCYQI -- YYDIVHEVAWEAEKEOGRELVSFFRKGW 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 -IPLSTDEV-----VEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 FQGSDLGMAEEA-ERPGE-----KAGQHSPLREE-----HVTCVQSILDEFLQTYGSL- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 FQGSDLGMAEEA-ERPGE-----KAGQHSPLREE-----HVTCVQSILDEFLQTYGSL- 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 KRHVL------TMDDLGTLYGONW---LNDQVMNMYGDLVMD 174
                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 782;
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                   APPLICANT: Schepmann, Hala G
TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
FILE REFERENCE: P02081US1
CURRENT APPLICATION NUMBER: US/10/041,007
CURRENT FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: US 60/259,881
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 782
                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-887-586A-46
Squence 46. Application US/09887586A
Fatent No. US20020094556A1
GENERAL INFORMATION:
APPLICANT: Chappell, Joseph
APPLICANT: No. US20020094556A11, Joseph P.
APPLICANT: Starks, Courtney M.
APPLICANT: Manna, Kathleen R.
TITLE OF INVENTION: SYNTHASES
FILE REFERENCE: 07678-025001
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 09/398,395
PRIOR PILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 60/130,628
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 60/150,262
PRIOR PILING DATE: 1999-08-23
NUMBER OF SEC ID NOS: 58
SSCTWARE: FRALESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.4%; Score 78.5; Dest Local Similarity 23.4%; Pred. No. 15; Matches 40; Conservative 32; Mismatches
APPLICANT: Matsuda, Seiichi P.T.
                                                                                                                                                                                                                                                                                     ; TYPE: PRT; ORGANISM: Ables grandis
US-10-041-007-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Abies grandis
US-09-887-586A-46
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1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                       score:
                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB s
Maximum DB s
                                                                                   OM protein
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database
                                                                                                                                                                                                              Title:
Perfect
                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	ı	% Query			SUMMARIES	
No.	Score	Match	Length	DB	ID	Description
1	91.5	5.2	654	4	US-09-090-793-2	
7	91.5	5.2	661	7	US-08-375-709-3	Sequence 3, Appli
m	91.5	5.5	661	Н	US-08-752-929-3	'n
4	98	4.9	727	4	US-09-134-001C-4067	406
S	83	4.7	1151	4	US-09-134-001C-3242	3242,
9	82.5	4.7	343	Н		56,
7	82.5	4.7	343	4	US-08-474-853-56	56,
80	82.5	4.7	343	4	'n	56,
6	82.5	4.7	343	S	PCT-US94-02629-56	56,
10	82.5	4.7	451	4	US-09-357-251-35	35,
11	82.5	4.7	674	4	US-08-961-083-200	200
12	82	4.6	353	~	US-08-034-650-11	11,
13	82	4.6	353	Н	US-08-449-015-11	Sequence 11, Appl
14	81.5	4.6	200	Н	083-6	68
15	81.5	4.6	633	m	US-09-041-991A-10	10
16	81	4.6	407	m	US-08-989-370-6	9
17	81	4.6	899	4	US-09-134-001C-4816	481
18	81	4.6	2987	7	US-08-970-269A-29	
19	81	4.6	2987	4	US-09-407-562-29	29,
20	81	4.6	3959	7	US-08-970-269A-30	30,
21	81	4.6	3959	4	US-09-407-562-30	30,
22	0	4.5	449	4	US-09-134-001C-5673	567
23	σ	4.5	332	7	US-09-057-762-7	
24	79.5	4.5	332	m	-9	,
25	g,	4.5	882	4	US-09-342-648-9	δ
56	$\sigma$	4.5	1010	4	US-09-134-001C-5178	5178,
27	œ	4.4	436	9	943-	

Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli
64,	16,	46,	13,	38,	40,	42,	13,	38,	40,	42,	27,	27,	27,	27,	23,	'n	Z,
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-914-375C-64	US-09-360-545-16	US-09-398-395A-46	US-09-234-393-13	US-09-234-393-38	US-09-234-393-40	US-09-234-393-42	US-09-865-171-13	US-09-865-171-38	US-09-865-171-40	US-09-865-171-42	US-08-599-171A-27	US-08-646-590B-27	US-09-069-226-27	US-09-412-184-27	US-09-457-040B-23	US-08-288-408-5	US-08-655-782-5
4	4	4	4	4	4	4	4	4	4	4	7	7	٣	4	4	Н	4
450	782	782	817	817	817	817	817	817	817	817	453	453	453	453	538	678	678
4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4
78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78.5	78	78	78	78	78	7.8	78
	σ.	_	_	C)	<u></u>	<b>~</b> #	'n		37	<u>~</u>	σ.	_	_	~	13	_	ıc

ALIGNMENTS

RESULT 1 US-09-090-793-2 Sequence 2, Application US/09090793 Sequence 2, Application US/09090793 Patent No. 6140486 GENERAL INFORMATION: TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression TITLE OF INVENTION: Production of polyunsaturated fatty acids by expression TITLE OF INVENTION: Of polyketide-like synthesis genes in plants FILE REFERENCE: CGNE. 13. 0105 CURRENT PILLICATION NUMBER: US/09/090, 793 CURRENT PILLIG DATE: 1998-06-04 EARLIER APPLICATION NUMBER: 60/048,650 EARLIER FILLIG DATE: 1997-06-04 NUMBER OF SEO ID NOS: 66 SOFTWARE: PatentIn Ver. 2.0 SEO ID NO 2.
TYPE: PRT
; ORGANISM: Shewanella putrefaciens US-09-090-793-2

21; 135 RGF----RVAYKRHV------LTMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173 334 NAFGODVEVLFASHSAPVWGNQAINDFLRLQRDNYGLVHNQTLRLANDGVGIQDIGDAIQ 393 54 AERPGEKAGQH-----SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLED 103 104 IFQQEFST------PSRKGLVLQLIQSYQRMPG------NAMV 134 174 DIVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232 233 RRTITYFDSQRTLNRRCP--KHIAKYLQ-----AEAVKKDRLDFHQGWKGYF-----KMN 280 1 MYS----AQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLG----MAEE 53 Query Match 5.2%; Score 91.5; DB 4; Length 654; Best Local Similarity 21.2%; Pred. No. 0.5; Matches 78; Conservative 43; Mismatches 118; Indels 129 426 ò g δy qq δ qq Ωÿ qq δy Dp öλ QQ

281 VARQNNDS 288

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APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Akiko
APPLICANT: YAMADA, Akiko
APPLICANT: KATO, Selshi
APPLICANT: KATO, Selshi
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding for Elcosapentaenoic Acid Synthesizing
TITLE OF INVENTION: Enzymes and Process for Production of Eiscosapentaenoic
TITLE OF INVENTION: Acid
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
336 NAFGQDVEVLFASHSAPVWGNQAINDFLRLQRDNYGLVHNQTLRLANDGVGIQDIGDAIQ 395
                                                174 DIVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232
                                                                                                                                            233 RRTITYFDSQRTLNRRCP--KHIAKYLQ-----AEAVKKDRLDFHQGWKGYF-----KMN 280
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.2%; Score 91.5; DB 1; Length 661; Best Local Similarity 21.2%; Pred. No. 0.51; Matches 78; Conservative 43; Mismatches 118; Indels 129;
                                                                               COUNTRY: USA
ZIP: 2007-5109
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-NOV-1996
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,709
FILING DATE: 20-0AN-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/752,929
20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08752929
Patent No. 5798259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 534
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25,258
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
US-08-752-929-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                   281 VARQNNDS 288
                                                                                                                                                                                                                                                                                                 484 MAEPENDS 491
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STATE: D.C
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US-08-752-929-3
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                                                                                                                                                                                                                  APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Kazunaga
APPLICANT: YAZAWA, Akiko
APPLICANT: KATO, Selashi
APPLICANT: KONDO, Kiyosi
TITLE OF INVENTION: Gene Coding For Eicosapentaenoic Acid
TITLE OF INVENTION: Synthesizing Enzymes and Process for Production of
TITLE OF INVENTION: Eiscosapentaenoic Acid
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 AYQYGATLGKHDHGIVDAALGKGLSKGEITYVAP--DYTLNSEGKWETLT----IDGLEM 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 IYSHSHADHFGGA-----RGVQEMFPDVKVYGS-----DNITKEIVDENVLAGNAMSRRA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 AERPGEKAGQH-----SPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLED 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 RGF----RVAYKRHV------LIMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 91.5; DB 1; Length 661;
21.2%; Pred. No. 0.51;
tive 43; Mismatches 118; Indels 129; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MYS---AQRFWGTIWARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLG----MAEE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 IFQQEFST-----PSRKGLVLQLIQSYQRMPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25,258
FR: 53466/150/AAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,709
FILING BATE: 20-JAN-1995
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAX-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: JP 4-147945
APPLICATION NUMBER: JP 4-147945
ATTICH DATE: 15-MAX-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            Sequence 3, Application US/08375709
Patent No. 5683898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2*
Best Local Similarity 21.2*
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: WEGNER, Harold C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-375-709-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
                                                                                                                                                                                                GENERAL INFORMATION:
     :| | | | 1 | 482 MAEPENDS 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                     US-08-375-709-3
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Sequence 3242, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: UUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .026 --IHVIINAKFNVEPSLVDTALLQIELNSMLQSLPKQLTKRKIVNPKSQKDIQV----- 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED TITLE OF INVENTION: THEREON NUMBER OF SEQUENCES: 62 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 CPKHI---AKY-LQAEAVKKDRLDFHQGW-----KGYFKMNVARQNNDSDCGAFVLQYC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVK-----RWTKN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 VDIFNKE-----LLLIPIH--LEVHWSLISVDVRRRTITYFDSQ------RTLNRR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 VEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGN--AMVRGF-----RVAYKRHVLTMDD 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    861 INELRESIQYFAKVESRTILEQQMTYQLQQMNNSFKKMIKDFHDDNAKLSARQH-----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1151;
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.7%; Score 83; DB 4; Best Local Similarity 22.4%; Pred. No. 10; Matches 59; Conservative 46; Mismatches 94
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR PRICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR PILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56, Application US/08180209B Patent No. 5593877 GENERAL INFORMATION:
APPLICANT: King, Te-Piao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1078 -HIA-NQTLELLQDDLNSLRRQL 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 KHLALSQPFSFTQQDMPKLRRQI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 Hackensack Avenue
     RIFNFPFYF -----RGEVY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hackensack
                                                                         RESULT 5
US-09-134-001C-3242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-134-001C-3242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-180-209B-56
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     202
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TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: UNMBER: US/09/134,001C
CURRENT APPLICATION UNMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 727
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                                                                                                                               135 RGF----RVAYKRHV-----LTMDDLGTLYGQ--NWLNDQV-MNMYGDLVM 173
                                                                                                                                                                                                                                                                                                                              | : | : | : | : | : | 336 NAFGQDVEVLFASHSAPVWGNQAINDFLRLQRDNYGLVHNQTLRLANDGVGIQDIGDAIQ 395
                                                                                                                                                                                                                                                                                                                                                                                             DIVPEKVHFFNSFFYDKLRIKGYDGVKRWTKNVD-IFNKELLLIPIHLEVHWSLISVDVR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                             427
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                                                173 IYSHSHADHFGGA----RGVQEMFPDVKVYGS-----DNITKEIVDENVLAGNAMSRRA 222
                                                                                                                                                                                                 ----NAMV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 MPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFF 187
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4.9%; Score 86; DB 4; Length 727;
Best Local Similarity 18.7%; Pred. No. 2.3;
Matches 49; Conservative 46; Mismatches 93; Indels
                                                                                                                                                                                                 --PSRKGLVLQLIQSYQRMPG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4067
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Te Piao KING
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
TITLE OF INVENTION: THERAPIES BASED THEREON
TITLE OF INVENTION: THERAPIES BASED THEREON
TITLE OF INVENTION: THERAPIES BASED THEREON
CURRENT APPLICATION NUMBER: US/09/166,205B
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PASLESEQ for Windows Version 3.0
SEQ ID NO 56
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 ----GDLV------MDTVPEKVHFFNSFFYDKLRTKGYDGV-----KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR------ 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 -LFMEETLKAAKRMRPA----ANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKM 211
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nilarity 19.5%; Pred. No. 1.7;
Conservative 43; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.7%; Score 82.5; DB 4;
Best Local Similarity 19.5%; Pred. No. 1.7;
Matches 46; Conservative 43; Mismatches 70;
                                                                                                                                                                                                                                     600-1-074 CIPB
                        APPLICATION NUMBER: US 08/180, 209
FILING DATE: 11-JAN-1994
FRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/031,400
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                                                                                                                     FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 343 amino acids
                                                                                                                                                                                                                                                                                                                                       TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
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US-09-166-205B-56
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STRANDEDNESS: sin
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Matches 46; Conserv
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US-08-474-853-56
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TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber 6 Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 -LFWEETLKAAKRMRPA----ANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKM 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 82.5; DB 1; Length 343; 19.5%; Pred. No. 1.7; tive 43; Mismatches 70; Indels 7
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,853
FILING DATE: O7-JUN-1995
CLASSIFICATION: 436
                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIP
TELECOMUNICATION INFORMATION:
TELEPAX: 201 487-5800
TELEFAX: 201 343-1684
ITELEX: 133521
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                   APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-7An-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
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CITY: Hackensack
STATE: New Jersey
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CURRENT APPLICATION DATA:
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MOLECULE TYPE: peptide
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US-08-180-209B-56
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                                                         212 ELLLIPIHLEVHWS-----LISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                162 -LEMEETLKAAKRMRPA-----ANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKM 211
                                                                                                                                      266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPF----SFTQQDMPKL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 451;
                                                                                  116 -----PIFRQ-NWASLQPYKKLSVEVVRREHPFWDDQR-VEQEAKRRFEKXGO
| :: | : | : | : | 64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 LPSE-NYAENDFYDLVRTIGGDLVEK----VPLIDKF-----VHPKTH----
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 82.5; DE; Pred. No. 2.6; 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236 ----ITYFDSQRTLNRRCPKHIAKYLQAEAVK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/357,251
CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60/093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRVAYKRHVLTMDDLGTLYGQNWLND----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 200, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                     US-09-357-251-35; Sequence 35, Application US/09357251; Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Office 97
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-357-251-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maryland
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-961-083-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                             Sequence 56, Application PC/TUS9402629
GENERAL INFORMATION:
APPLICANT: King, Te-Piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: YEALURONIDASE, AND IMMUNOLOGICAL THERRAFIES BASED THEREON
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                              ELLLIPIHLEVHWS-----LISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD 265
                                                                                                                     -----PIFRQ-NWASLQPYKKLSVEVVRREHPFWDDQR-VEQEAKRRFEKYGQ------ 161
                    ---KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 ----GDLV------MDTVPEKVHFFNSFFYDKLRTKGYDGV-----KRWTKNVDIFNK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                 77;
                                                   64 KDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 NAMVRGFRVAYK-----RHVLTMDDLGTLYG--QNWLN----DQVMNMY-
                ----GDLV-------MDTVPEKVHFFNSFFYDKLRTKGYDGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.7%; Score 82.5; DB 5;
19.5%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600-1-074 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROCR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-0AN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESQ., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US94/02629
10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 343 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 201 487-5800
201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
STATE: New Jerse
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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99 EKLEDIFQQEFSTPSRKGL-VLQLIQSY----QRMPGNAMVRGFRVAYKRHVLTMDDLGT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 LYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKEL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 SDLGMAEEAERPGEKAGQHSPL-----REEHVTCVQSILDEFLQTYGSLIPLSTDEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 LLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 353;
                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.8%; Prec. ....
                                                                                                                                                                                                                                                                                                             NAME: Kokulis, Paul N.
REGISFRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1615 L. Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2IP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08449015
Patent No. 5804409
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 353 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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20036-5601
                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EKLED---IFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 ESEGMFYFHILGDSYYEKVYDNVSIFENLYET-------QEMKSFALISAWGK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AYKRHVLTM--DDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 LYKARLFEQLRFDIGKLGEDGYLNQKVY------LLSEKVIYLNKSLYAYRIRKG-- 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 GVKR-WTKN-----VDIFNKELLLI-----PI--HLEVHWSLISVDVRR------RTIT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 SLSRVWTEKWMHALVDAMSERITLLANMGYPLEKHLAVYRQMLEVSLANGQASGLSDTAT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08034650
Patent No. 5641671
GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VISSEN, Cornelis T.
APPLICANT: PRODUCTION. OF ACTIVE PSEUDOMONAS GLUMAE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 EAERPGEKAGQHSPLRE---EHVTCVQS---ILDEFLQT-YGSLIPLSTDEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 674;
                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.7%; Score 82.5; D
Best Local Similarity 22.1%; Pred. No. 4.9;
Matches 56; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: CUSHMAN, DARBY & CUSHMAN: 1615 L. Street, N.W. Washington
                                                                                                                                                                      APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION UNDRER: 36,373
REFERENCE/DOCKET UNDBER: PB34
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8504
TELEFAN: (301) 309-851
INFORMATION FOR SEQ ID NO: 200:
                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 674 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
  ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-961-083-200
                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : || ||:
259 YKEFEMKQRLLNQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 YFD---SQRTLNR 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-08-034-650-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-587
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 19.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 KGYFKMNVARQNNDSDC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSILOMNGCHIXNFNXC 285
                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                          ) NAME/KEY: Protein

) LOCATION: 1.500

OTHER INFORMATION:

) OTHER INFORMATION:

US-08-117-083-68
                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-041-991A-10
                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 LYGQNWLNDQVWNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKEL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 EKLEDIFQQEFSTPSRKGL-VLQLIQSY----QRMPGNAMVRGFRVAYKRHVLTMDDLGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 SDLGMAEEAERPGEKAGQHSPL -----REEHVTCVQSILDEFLQTYGSLIPLSTDEVV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68, Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E. APPLICANT: Inqlis, Stephen C. APPLICANT: Munro, Alan J. TITLE OF INVENTON: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 LLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.6%; Score 82; DB 1
Best Local Similarity 20.8%; Pred. No. 2;
Matches 48; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Walter H. Dreger
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                    REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEPRA: (202) 861-3000
TELEFAX: (202) 822-0944
TELER: (5714627 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,015
FILING DATE: 24-MX-1995
CLASSIFICATION: 435
                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     353 amino acids
                                                                                                                                                                          NAME: Kokulis, Paul N. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-449-015-11
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                                                                                                                                                                                                                                                                                                                                                                     amino acid
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-117-083-68
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                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 VLCISVRRKRTSSTRVDSSRYINLGMRLPRHTCALSKWKDAVVLCLQIGQNHGIWILMVS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 YORMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 FLQTYGSLIPLSTDEVVEKLEDIFQ------QEFSTP-----SRKGLVLQLIQS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 SFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPI-HLEVHWSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 SELQAGESVKFGNSINVKHTSVSAKQLRTRIRQQ-----LPLYSHLLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                           /note= "Xaa refers to stop codon in
the open reading frame."
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Patent No. 6107278

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....r Pes
STREET: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 81.5;
19.8%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin CUSKENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,991A
FILLIG DATE: 13-MAR-1998
A-58783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 YQRMPGNAMVRGFRVAYKRHV-LTMDDLG----TLYG-QNWLNDQVMNMYGDLVMDTVPE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| | : :| | : :| | 174 ----LPLFAQAANIHLSYIRDVILNAEEWGISAATLRTYONHLRNYTRD-YSNYCIDTYQT 229
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ASILISNVCS-IGDHVAQEL----FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                        Query Match
4.6%; Score 81.5; DB 3; Length 633;
Best Local Similarity 23.2%; Pred. No. 5.7;
Matches 52; Conservative 33; Mismatches 96; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AFRGLNTRIHDMLEFRTYMFLNVFEYVSIWS----LFKYQSLLV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KVHFFNSFFYDKLRTKGY-----DGVKRWTKNVDIFNKELLLI 216
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERROKE/DOCKET NUMBER: MA-709
TELECOMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPRONE: (352) 375-8100
TELEPRONE: (352) 375-8100
TELEPRONE: (352) 375-5800
INFORMATION FON SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 amino acids
TYPE: amino acids
STRANDEDNESS: single
STROPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-991A-10
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Search completed; December 16, 2002, 19:28:42 Job time :  $39\ \mathrm{secs}$ 

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December 16, 2002, 19:28:00 ; Search time 899 Seconds (without alignments) 49.209 Million cell updates/sec
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20: /SIDS2/gcddta/geneseqy/geneseqp-embl/AA1999.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                             1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_101002:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                            US-09-848-852A-3
1772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                Title:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human fetal brain	Human polypeptide	Human polypeptide	Human polypeptide	Amino acid sequenc	Human polypeptide	Human ovarian anti	Human protein sequ	Human polypeptide	Human protein sequ
IES													
SUMMARIES			ut 	-	AAM39269	AAM41055	AAM41056	AAB31977	AAM39270	ABP41139	AAM25617	AAO04440	AAB92493
			a :	21	22	22	22	22	22	23	22	22	22
			e Match Length DB	371	371	438	438	568	354	309	270	119	191
	oР	Query	Match	94.1	94.1	94.1	94.1	94.1	88.0	83.0	44.1	34.7	27.7
			score	1667	1667	1667	1667	1667	1558.5	1470	781.5	614.5	490
		Result	. ON .	-	7	Э	4	S	9	7	8	6	10

98US-0082904. 98US-008894. 98US-0089278. 98US-0091647. 98US-0097639.

> 11-JUN-1998; 12-JUN-1998; 02-JUL-1998; 24-AUG-1998; 22-APR-1999;

(ALPH-) ALPHAGENE INC

99WO-US08504

23-APR-1999;

04-NOV-1999

24-APR-1998;

Homo sapiens WO9955721-Al

gene therapy

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amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                            2001-442253/47.
                                                                                                                                                                                                                                                                                           Liu C, A
Wang Z, W
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 AA;
                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAI58425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.N.S disorders.
                                                                          WO200153312-A1
                                                                                                                                                                                                    03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification
                                                    Homo sapiens.
                                                                                                                            26-DEC-2000;
                                                                                                                                                                              09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                  25-APR-2000;
                                                                                                    26-JUL-2001
                                                                                                                                                                                                                                                                                           Tang YT,
Wang J, F
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                    This invention describes novel human secreted proteins which are encoded by polynucleotides obtained from fetal brain, adult skin, adult brain, adult thymus and adult aorta cDNA libraries. The calult heart, adult thymus and adult aorta cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, hemostryity, immune stimulating cettivity, tissue growth activity, hemostratic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The polynucleotides are also stated to be useful for gene therapy.

ANYSO905-YSO947 represent the secreted proteins described in the method of the invention which are encoded by the polynucleotides represented in
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                                                    human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
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  Rapiejko
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100.0%; Pred. No. 7e-157;
ive 0; Mismatches 0;
 Hall J,
                                                                                                               Claim 21a; Page 223-225; 282pp; English.
 Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM39269 standard; Protein; 371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 314; Conservative
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  Yuan
                        WPI; 2000-052801/04
                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     371 AA;
                                     N-PSDB; AAZ43782
                                                                                                                                                                                                                                                                                                                                            AAZ43777-Z43808
 Valenzuela D,
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
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the encoded polypeptides (AAM36842-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as and central nervous system diseases, uncon as Alzheimer's, Parkinson's disease, Huthington's disease, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/Inhibin activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and assays for receptor activity, arthritis and inflammation, leukaemias and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
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chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ren F, W
Zhang J;
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Yang Y,
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100.0%; Pred. No. 7e-157;
ive 0; Mismatches 0;
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO 2414; 10078pp; English.
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Wehrman T, Xu C,
Goodrich R, Drman
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
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Matches 314; Conservative
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specification.
                             Sequence
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Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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          259 AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                           The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for treating disorders
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Zhang J;
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Yang Y,
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Drmanac RT;
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                                                                                                                                                                       AAM41055 standard; Protein; 438 AA
                                                                                                                                                                                                                                                                Human polypeptide SEQ ID NO 5986.
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Wehrman T, Xu
Goodrich R,
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2000US-052317.
2000US-052317.
2000US-0623312.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
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                                                                                                                                                                                                                                  (first entry)
                                                                     RQIYKELCHCKLTV 332
                                                                                   WPI; 2001-442253/47.
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Wang Z,
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14-SEP-2000;
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29-NOV-2000;
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Zhao QA,
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305 VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ 364
                                                                                                                                   LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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                                                                                                                                                                                                                                                                                                                245 VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 304
                                                   Gaps
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                                                                             19 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                     AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR
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                         Length 438;
                                                   Indels
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Yang Y,
                      94.1%; Score 1667; DB 22;
100.0%; Pred. No. 8.9e-157;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic;
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM41056 standard; Protein; 438
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2000us-0552317.
2000us-0598042.
2000us-065342.
2000us-0653450.
2000us-0653450.
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                                     Best Local Similarity 100.
Matches 314; Conservative
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Wang Z,
Zhou P,
AA;
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09-JUL-2000;
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14-SEP-2000;
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Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM41056;
                         Query Match
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Zhao
                                                                                                                                   79
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WO200109292-A2
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AAM39270
ID AAM3'
XX
AC AAM3'
XX
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                                                                                                The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system is as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinty inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and the NS disorders.
                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            125 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 184
                                                                                                                                                                                                                                                                                                                                                                                                     LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1; sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyehocytic leukaemia.
                                  polypeptides, useful for treating disorders system injuries -
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                    Length 438;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                 94.1%; Score 1667; DB 22;
100.0%; Pred. No. 8.9e-157;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a human SENP3 polypeptide.
                                                                            Example 2; SEQ ID NO 5987; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31977 standard; Protein; 568 AA.
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                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 314; Conservative
                                    Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 RQIYKELCHCKLTV 438
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 WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                         438 AA;
            N-PSDB; AAI60212
                                                                                                                                                                                                                                                                                                 specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB31977;
                                                                                                                                                                                                                                                                                                                          Sequence
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The present sequence represents human de-sentrinase (SENP) 3 polypeptide. The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleus. SENP3 is found in both locations. SENP3 is found in both locations. SENP3 is found in both locations. SENP3 is found in both locations. SENP3 polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins modified by ubiquitin or NEDB8. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cycomegaLovirus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polynucleotides are used as hybridisation probes and amplification primers for detecting gene expression or preparing mutated sequences, also as antisense sequences for inhibiting SENP expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQOEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding de-sentrinase polypeptides, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 568;
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Pred. No. 1.3e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 1121-122; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 antiproliferative or antiviral agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM39270 standard; Protein; 354 AA.
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100.0%; Pre
0; /
                                                     31-JUL-2000; 2000WO-US20884
                                                                                                             99US-0146774
                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM.
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                                                                                                                                                                                                                                                                                   WPI; 2001-182947/18.
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Matches 314; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 AA;
                                                                                                                                                                                                                              ETH;
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF54831
                                                                                                                                                                                                                              Yeh
                                                                                                             31-JUL-1999;
08-FEB-2001
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237

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VAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDG 198
                          ABP41139;
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ABP41139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system is near the asset of the peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification.
                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 354;
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Yang Y,
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Pred. No. 3.9e-146;
0; Mismatches .0;
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Xue AJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
                                                Human polypeptide SEQ ID NO 2415.
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2000US-0552317.
2000US-0620312.
2000US-062312.
2000US-062191.
2000US-0661191.
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  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                     WO200153312-A1,
                                                                                                                                                                                                                                                            Homo sapiens.
22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001
                                                                                                                                                                                                              leukaemia.
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Zhao QA,
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79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFR 138 

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ556305), and also encompasses polypeptides 90% identical and polynuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynuclectides, antibodies against human ovarian antigens, and the use of ovarian antigen polynuclectides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; infection; inf
                                                                                                                                              AEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLR 318
                                                                                                                                                                                          cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases
                                   VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ovarian antigen HOFOB27, SEQ ID NO:2271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                 neurological diseases
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antific lammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia;
anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia;
antiagregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
dermatological; antiallergic; antiababetic; cytostatic;
neuroprotective; antidepressant; nootropic; antiababetic; cytostatic;
munnostimulant; gene therapy; antisense therapy; vaccine; inflammation;
immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
antianaphylantic; rheumatorid arthritis; septic shock; pancreatitis;
genetic disease; haematopoletic disorder; platelet disorder; asthma;
thrombocytopania; osteoporosis; severe combined immunodeficiency;
allergic rhinitis; diabetes; multiple sclerosis; depression;
allergic rhinitis; diabetes; multiple sclerosis; depression;
allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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   syndrome, ovarian cysts, and dysmenorrhoea), endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 FSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 GMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 VDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 GHRRRGRAAGEKAGQHSPLREEHVTCVQSILDEFLQIYGSLIPLSTDEVVEKLEDIFQQE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLIS
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Pred. No. 2e-137;
0; Mismatches 8; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM25617 standard; Protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.0%;
97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 AA;
   polycystic ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
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AAM25966 to AAH99904 encode the human proteins given in AAM25225 to
AAM25963. The proteins can have activities based on the tissues and
calls they are expressed in, such as: antinflammatory; antirheumatic;
antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
cardiavascular; antianemnic; antiaggregant; heamostatic; vulnerary;
antidiabetic: osteopathic; dermatological; antiallergic; antiasthmatic;
antidiabetic: cytostatic; neuroprotective; antidepressant; nootropic;
antidiabetic: cytostatic; neuroprotective; antidepressant; nootropic;
antidiabetic: cytostatic; neuroprotective; antidepressant; nootropic;
cardiavastrisonian; and immunostimulant. The proteins and polynucleotides
encoding them can be used in gene therapy, antisense therapy and vaccine
production, The proteins and polynucleotides are useful for screening for
conding them can be used in gene therapy, antisense therapy and vaccine
production, and antigonists of a protein and for the treatment and diagnosis
of disorders associated with the activity of a protein e.g. inflammation,
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
andemia platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
andemia platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
conteoporosis, severe combined immunodeficiency, allores allores,
continuitis, asthma, diabetes, cancer, multiple sclerosis, depression,
and and an antigonis disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 FINREITNYRARHQKC---NFRIFYNKHMLDMDDLATLDGQNWLNDQVINNYGELIMDAV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GEKAGQHSPLREEHVT-CVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGONWLNDQVMNMYGDLVMDTV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 PDKVHFFNSFFHRQLVTKGYNGVKRWTKKVDLFKKSLLLIPIHLEVHWSLITVTLSNRII 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFYDSQGIHFKFCVENIRKYLLTEAREKNRLNL-QGWQTAVTKCIPQQKNDSDCGVFVLQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 PEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQ
                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 270;
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                                                                                                                                              99US-0471275.
2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
                                                                                                       22-DEC-2000; 2000WO-US35017
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Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders.
                                                                                                                                                                                                                                                                                                                           WPI; 2001-457603/49.
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                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAH99558
                  WO200153455-A2
                                                                                                                                                                       21-JAN-2000;
25-APR-2000;
                                                                                                                                                   23-DEC-1999;
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RESULT 9

Homo sapiens

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AAB92493 standard; Protein; 191 AA.
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    AAB92493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                    Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 GYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 KYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDM 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; SEQ ID NO 18332; 1399pp + Sequence Listing; English.
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85.2%; Pred. No. 5e-53;
live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
                     AA004440 standard; Protein; 119 AA.
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                                                                                                                                                       Human polypeptide SEQ ID NO 18332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKLRRQIYKELCHCK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLITITITITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                             WO200164835-A2.
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001.
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                                                                  AAO04440;
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AAO04440
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the 5-end sequence/3-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs. ARMO3166 to ARM13628 and AAM13633 to AAM1872 represent human cDNA sequences; and AAM13639 to AAM13632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to objugnucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K,
Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 10591; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
Human protein sequence SEQ ID NO:10591
                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000;
                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999;
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                                                                                                                                                                                                                                                                           07-FEB-2001
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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79 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 114

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RESULT 10

Wed Dec 18

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NQDEVLSEAFRL----TITRKDIQTLNHLNWLNDEIINFYMNMLMERSKEKGLPSVHAF 493
                                                                                                                                                                                     302 ALSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                   AAB31976 standard; Protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000; 2000WO-US20884
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 22.2;
Best Local Similarity 29.6;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-182947/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeh ETH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAF54830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200109292-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                      AAB31976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gong L,
 439
                                      184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents human de-sentrinase (SENP) 1 polypeptide. The specification describes SENP2 and SENP3 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleous, SENP3 is found in the nucleous, and SENP3 is found in both locations. SENP polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins modified by ubjquitin or NEDDB. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polymeted as a hybridisation probes and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 AELWIKELTSVYDSRARERLRQIEEQKALALQLQNQRLQER--EHSVHDSVELHLRVPLE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EE-HVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 MPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primers for detecting gene expression or preparing mutated sequences, also as antisense sequences for inhibiting SENP expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                            de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                             sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyelocytic leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PLR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide encoding de-sentrinase polypeptides, useful as antiproliferative or antiviral agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 ASILISNVCSIGDHVAQE----LFQGSDLGMAEEAERPGEKAGQHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human SENP1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 456; DB 22;
Pred. No. 3.2e-36;
156 LDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSR 191
                                                                                                              Ā.
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                                                                                                           AAB31973 standard; Protein; 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.7%;
34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-2000; 2000WO-US20884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0146774
                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-182947/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 AA;
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                   15-MAY-2001
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                                                                                                                                                 AAB31973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Best Local 9
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                                                                        RESULT 11
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301
                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; de-sentrinase; SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sentrin-specific protease; sentrin; anti-proliferative agent; anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation; PML; tumour suppressor; acute promyelocytic leukaemia.
                  244 TLNRRCPKHIAKYLQAEAVKKDRLDFH-QGWKGYFKMN-VARQNNDSDCGAFVLQYCKHL
NSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide encoding de-sentrinase polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a human SENP2 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 118-120; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiproliferative or antiviral agents -
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to stomach cancer-expressed genes (AAI93842-AAI93917) and the encoded proteins (AAM93967-AAM94039). The genes can be used as markers in blood tests for screening for the early stages of the disease. The proteins and peptides can be used as targets
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                                                                                     188
                                                                                                        363
                                                                                                                            248
                                                                                                                                               423
                                                                                                                                                                            New Stomach cancer-associated genes, useful as markers in blood tests for screening for the early stages of the disease \mbox{-}
                                              TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Aburatani
Midorikawa Y;
        13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV
                                                            --VSIIETKEKNCSGKERDRRTDDLLELTEDM-EKEISNALGHGPQDEILSS-----
                                                                                     133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
                                                                                                                                      ------GSNGLLRRK--
                                                                                                       ----AFKLRI-TRGDIQTLKNYHWLNDEVINFYMNLLVERNKKOGYPALHVFSTFFY
                                                                                                                           DKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRKTITYFDSQRTLNRR
                                                                                                                                                                 CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA
                                                                                                                                                                                                                                                                                                                                                        Human; stomach cancer; marker; screening; micro-metastasis;
                                                                                                                                                                                                                                                                                                                                    Human stomach cancer expressed polypeptide SEQ ID NO 92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 167-169; 242pp; Japanese
                                                                                                                                                                                                       303 LSQPFSFTQQDMPKLRRQIYKELCHCKL 330
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RDKPITFTQHQMPLFRKKWVWEILHQQL 508
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                                                                                                                                                                                                                                                                           AAM94011 standard; Protein; 589
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99JP-0300253.
99US-0159590.
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17-FEB-2000; 2000US-0183322.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                          231 SRRGYQLEP-
                                                                                                                                                                                                                                                                                                                                                                                                       WO200109317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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18-OCT-1999;
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Kodama T,
                                                                                                                                                                                                                                                                                              AAM94011;
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                                                                                                                                                                                                                                                                                 311 SRRGYOLEP-----GILSEEVSARLRIGS-------GSNGLLRRK-- 342
                                                                                                                                                                                                                                                                                                                                  TCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLA 302
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                    ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy,
                                                                                                                                                                                                                                                                                                                                                               | : | : | : : | : : | 343 --VSIIETKEKNCSGKERDRRTDDLLELTEDM-EKEISNALGHGPQDEILSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                          133 MVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK----VHFFNSFFY
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screening for compounds to treat the disease. They can also predicting micro-metastases. The gene can predict peritoneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                      90;
                                                                                                                                         Length 589;
                                                                                                                                                                                      Indels
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Otsuki
                                                                                                                           ; Score 393; DB 22;
; Pred. No. 5.2e-30;
64; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 LSQPFSFTQQDMPKLRRQIYKELCHCKL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95254 standard; Protein; 589
                                                                                                                                       22.2%;
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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09-JUN-2000; 2000JP-0241899
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                                                                                                                      Query Match
Best Local Similarity 29.6%;
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                                                                                        589 AA;
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                                                 dissemination.
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Myers EW;

Li PWD,

Venter JC, Adams M,

(PEKE ) PE CORP NY

WPI; 2001-656860/75.

N-PSDB; ABL03535

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2000US-191637P. 2000US-0614150.

23-MAR-2000; 11-JUL-2000;

23-MAR-2001; 2001WO-US09231

27-SEP-2001

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                                                                                                                          The present invention describes primer sets to 10 synumestating your comprises: (a) an oligo-dr primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in artisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the companion and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the connection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers are seen also useful for the cNAM assally without any specialised methods. AAH33618 for AAH33628 and AAH3632 to AAH3632 to AAH3622 to AAH36322 companion of the connection and connection and connection and connection and connection are used in the exemplification connection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 ARRGAHLAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes primer sets for synthesising 5602
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pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.2%; Score 393; DB 22; Length 589; 29.6%; Pred. No. 5.2e-30; Live 64; Mismatches 107; Indels 66
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Claim 8; SEQ ID 17423; 2537pp + CD ROM; English
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WO200171042-A2

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticidaes, therapeutics and pharmaceutical furges. The invention discloses genomic DNA sequences (ABLIGIT6-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
New isolated nucleic acid detection reagent for detecting 1000 \text{ or more} genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 AVKKDRLDFH-QGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRR 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 LIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHV-LT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 MDDLGTLYGQNWLNDQVWNMYGDLVMDTVPEK-----VHFFNSFFYDKLRTKGYDGVKR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 LIPL-TEEHHDRFNEITQDDKST----------EIIFKFNLHIT 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                 Disclosure; SEQ ID NO 5088; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 468;
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28.5%; Pred. No. 5.2e-22;
tive 55; Mismatches 85;
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Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    (ABB57737-ABB72072).
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Title: Perfect score:

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Scoring table: Sequence:

Searched:

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sequence 74, Appl Sequence 792, App Sequence 223, App Sequence 223, App Sequence 19, Appl Sequence 19, Appl Sequence 113, App Sequence 134, App Sequence 134, App Sequence 177, App Sequence 177, App Sequence 177, App Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 177, Appl Sequence 173, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 167, Appl Sequence 167, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178, Appl Sequence 178
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Corley, Nail C.
Guegler, Karl J.
Yue, Henry
Patterson, Chandra
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
          US-09-960-253-74

US-09-878-574-7902

US-10-008-461-1

US-09-728-445-223

US-09-294-093B-3098

US-09-956-004-58

US-09-924-401-19

US-09-783-590-788

US-09-925-302-171

US-09-925-302-171

US-09-815-242-942

US-10-063-547-139
                                                                                                                                                                     US-10-036-342-44

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US-09-973-451-38

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US-09-915-242-1

US-09-954-531-177

US-09-954-531-177

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US-09-918-497-42

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US-09-918-497-42

US-09-918-33

US-09-918-38-39

US-09-815-242-167

US-09-918-128

US-09-918-128-1280

US-09-918-128-1280

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/848,852A
FILING DATE: 07-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/09848852A Patent No. US20020106373A1 GENERAL INFORMATION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
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1710, Ap
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Sequence 835, App
Sequence 1710, Ap
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                                                                                               2002, 20:11:20 ; Search time 98 Seconds (without alignments) 1339.725 Million cell updates/sec
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                                                                                                                                                       US-09-848-852A-3
1772
1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                    OM protein - nucleic search, using frame_plus_p2n model
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US-09-983-965-835
US-09-777-564-1710
US-09-856-247A-1
                                                                                                                                                                                                                                                                                                                                hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     355320 seqs, 197730502 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Match Length
                                                                                                December 16,
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Result 8

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332
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Matches:
Conservative:
Mismatches:
Indels:
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                   ATTOREXY CALLS.

ATTOREXY LACY J.

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0515 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1991 base pairs
                                               as
      APPLICATION NUMBER: 09/069,725 FILING DATE: <Unknown>
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                                                                                                    TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ
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1772.00
100.00%
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PRIOR APPLICATION DATA
                                                                                                                     FOPOLOGY: linear
                                                                                                                                           CLONE: 2056178
                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                     LIBRARY:
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DB:
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Sequence 835, Application US/09983965
; Sequence 835, Application US/09983965
; Patent No. US202013716041
; GENERAL INCORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
; APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
SPOINT RELING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NOS: 5912
                                                                                                         ValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHis 300
                                                                                                                                                                                                                                                                                                 LeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGln 320
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                                                                                                                                                                                                                                                     28 IleSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ArgGluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGlnThrTyrGly
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                321 IleTyrLysGluLeuCysHisCysLysLeuThrVal 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.19e-83
704.00
97.86%
96.43%
39.73%
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ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
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                                                                           GluPheSerThrProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArg 127
                                                                                                                       MetProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysArgHisValLeuThr 147
                                                                                                                                            72
ValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysPro
                                 SerLeuIleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 LeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIlePheAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysGluLeuLeuLeulleProlleHisLeuGluValHisTrpSerLeuIleSerValAsp
                                                                                                                                                                                                                               Sequence 1710, Application US/09777564

Patent No. US2002022591A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Marmion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
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Matches:
Conservative:
Mismatches:
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661.50
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; ORGANISM: Homo sapiens
US-09-777-564-1710
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                                                                                                                                                                                                            RESULT 3
US-09-777-564-1710/c
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LENGTH: 503
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DB:
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           311
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APPLICANT: Lima, Christopher
APPLICANT: Mossessova, Elena
APPLICANT: Mossessova, Elena
TITLE OF INVENTION: Structure-Based Drug Design for Ulp1 Protease Substrates
FILE REFERENCE: 2650/1G681-US1
CURRENT APPLICATION NUMBER: US/09/856,247A
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 60/205,336
PRIOR APPLICATION NUMBER: 60/205,336
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
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              ArgGlyPheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeu 154
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GlnGlnAspMetProLysLeuArgArgGlnIleTyrLysGluLeuCysHisCysLysLeu
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Matches:
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                                                                                                                                                     Sequence 1, Application US/09856247A Patent No. US20020151028A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Saccharomyces cerevisiae
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                                        GGAGAAGACTTT------GATTTGATTCATTTAGATTGTCCGCAGCAACCA 1725
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                         211 LysGluLeuLeuLeuIleProIleHisLeu---GluValHisTrpSerLeuIleSerVal
                                                                           AspValArgArgArgThrIleThrTyrPheAspSer------GlnArgThrLeu
                                                                                                                             246 AsnArgArgCysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4735, Application US/09867701
Fatent No. US2002013237a1
GENERAL INFORMATION:
APPLICANT: Adjate, Paul A.
APPLICANT: Adjate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT FAPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 7902, Application US/09878574
Sequence 7902, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants
TITLE OF INVENTION: Diants
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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                                                                                                                                  GENERAL INC. 02.202201201301301
APPLICANT: Benson, Darin R.
APPLICANT: Monamath, Raodoh
APPLICANT: Lodes, Michael J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.556
CURRENT FILIANG DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 187
SOFTWARE: FASTSEQ for Windows Version 4.0
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Conservative:
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Indels:
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                                                                   US-09-960-253-74
; Sequence 74, Application US/09960253
; Patent No. US20020123619A1
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53.70%
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; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-960-253-74
425 AAGGAGCTG 433
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                   ---ArgThrLysGlyTyrAspGly-------ValLysArgTrpThrLys 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                 225 SerLeulleSerValAspValArgArgArgThrIleThrTyrPheAspSerGlnArgThr 244
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                                                                                                                                                                                                                                                         US-09-848-852A-3 (1-332) x US-09-878-574-7902 (1-264)
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Matches:
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Patent No. US20020127692a1
GENERAL INFORMATION:
APPLICANT: Barbara ink
APPLICANT: Alan Lewis
TITLE OF INVENTION: New Protein
FILE REFERENCE: QG1034(p80209)
CURRENT APPLICATION NUMBER: US/10/008,461
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 0027905.9
PRIOR FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
                                                                                                                                                    Length:
                                                                     ORGANISM: Glycine max
COTHER INFORMATION: Clone ID: 701100484H1
US-09-878-574-7902
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122.50
40.408
24.248
6.918
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 7902
LENGTH: 264
                                                                                                                                               2.7e-08
130.50
52.50%
33.75%
7.36%
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; LOCATION: (1)..(636)
US-10-008-461-1
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Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                    Alignment Scores:
Pred. No.:
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                                                            TYPE: DNA
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343 TTTTTCATTATGATTCCCATAGCAGGAGCAACTACAGTTCACGCAAAGCAGGTAGCAGAG 402
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Patent No. US30020102543A1

GENERAL INPORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 TyrLeuGlnAlaGluAlaValLysLys---AspArgLeuAspPheHisGlnGlyTrpLys
                                                                                                                                                                          ::: ||||::: ||||||| :::::: |||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: |||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: ||||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||::: ||::: |||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: |
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Mismatches:
Indels:
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                                                                                                                    179 LysValHisPhePheAsnSerPhePheTyrAsp-----
Length:
Matches:
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SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 223
LENGTH: 100
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US-09-728-445-223
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Best Local Similarity:
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Alignment Scores:
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                                                                                        APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Sherman, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYVUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL PROGRAM
SEQ ID NO 3098
LENGTH: 263
TURENT: LANGER OF SEQ ID NOS: LANGER OF SEQ ID NO 3098
LENGTH: 263
TURENT: LANGER OF SEQ ID NOS: LANGER OF SEQ ID NO 3098
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Patent No. US2002072595A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands
FILE REFERENCE: P832AD1
CURRENT FILING DATE: US/09/956,004
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 08/976,259
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 AGAGTAATCAACACCAGTTTGTGGCATGAAGAGCTAGTTGATATTCCTTTACAGCGGAAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAACTCAITGAAIGCGAIAAAATATITGTCCCTGIGCAIAAAAGAIGTACATIGGIGITA
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                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700347190H1
US-09-294-093B-3098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
21
19
45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
200 LysArgTrpThrLysAsnValAspIlePheAsnLysGlu 212
                  Length:
Matches:
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110.00
47.068
24.718
6.218
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Best Local Similarity:
Query Match:
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ORGANISM: Zea mays
                                                                               US-09-294-093B-3098
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1350 CTATITICCCTCGCTCGCCTAGGTATTGTGACGATGTTCGAACAACGACTTTGGTGAAT 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 GluLysLeuGluAspIlePheGlnGluPheSerThrProSerArgLysGlyLeuVal 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArg 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 ValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsn 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------AspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 LeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAsn 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 ArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                               ength:
PRIOR APPLICATION NUMBER: 60/031,626
PRIOR FILING DATE: 1996-11-22
NUMBER OF SEQ ID NOS: 142
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 58
LENGTH: 4835
TYPE: DNA
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31.69%
20.77%
6.09%
                                                                                                                                                                                                        ; ORGANISM: Escherichia coli
US-09-956-004-58
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Best Local Similarity:
Query Match:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GlyTyrAspGlyValLysArgTr 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 AAATCATGAAACAACTAATCTGTCAATACAGCAAAACGGCATGGGAGA-GTAAAAACATG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 oGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLys-----
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Patent No. US20020142957A1

GENERAL INFORMATION:

APPLICANT: Hepler, William T.

APPLICANT: Jiang, Wudiu

APPLICANT: Diang, Wudiu

TITLE OF INVENTION: AND DIANGOSIS OF COLON CANCER

FILE REPRENCE: 210121.550

CURRENT APPLICATION NUMBER: US/09/924,401

CURRENT FILING DATE: 2001-08-07

NUMBER OF SEQ ID NOS: 85

SEQ ID NO 19

LENGTH: 547
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30
21
24
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7988, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION: APPLICANT: Dillon, Patrick J. APPLICANT: Haseltine, William A.
                                                                                                                                                                                                                                                                                                                                                                                                      0.00034
103.00
53.12%
31.25%
5.81%
                                                        1971 GATGAAGAGTGC 1982
                                     287 AspSerAspCys 290
                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-924-401-19
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Best Local Similarity:
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US-09-783-590-7988
                                                                                                       US-09-924-401-19/C
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PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR PAPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SEQ ID NO 7988
LENGTH: 472
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NAME/KEY: misc feature
LOCATION: (226)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc feature
LOCATION: (263)
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NAME/KEY: misc feature
LOCATION: (382)
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OTHER INFORMATION: n equals
NAME/KEY: misc feature
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LOCATION: (330)
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LOCATION: (354)
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LOCATION: (240)
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LOCATION: (370)
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LOCATION: (387)
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LOCATION: (396)
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LOCATION: (406)
                                                                                                                                                                ORGANISM: Homo sapiens
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OTHER INFO
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                                                                                                                                               TYPE: DNA
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APPLICANT: Rosen et al
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                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnMetTyrGly---AspLeuValMetAspThrValProGluLysValHisPhePheAsn 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTATGGTATGGGTGGAGCTGGATNATGGGTGNCATTCCCCAGTNCAAAAGTTTCACTTCC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 TICAAACANGCTITITITICCAINAGACANGTIGGGITAANCCCAAAGGGGTINITAAI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etAspAspLeuGlyThrLeuTyr---GlyGlnAsnTrpLeu-AsnAspGlnValMet---
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41
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                     LOCATION: (447)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
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                                 OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (437)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (439)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                    OTHER INFORMATION: n equals a,t,g, or NAME/REY: misc feature
LOCATION: (450)
OTHER INFORMATION: n equals a,t,g, or NAME/REY: misc feature
LOCATION: (452)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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US-09-925-302-171
US-09-925-302-171
Sequence 171, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
                                                                                                                                  LOCATION: (442)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (427)
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1909-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 171
LENGTH: 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 MetAspThrValProGluLysValHisPhePheAsnSerPhePheTyr----
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36.79%
21.38%
5.28%
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US-09-925-302-171
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Best Local Similarity:
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269
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764 CTCTTTTTCCAAATTAGGGATGATTATGCTAATCTACACTCCAAAGAATATAGTGAAAAC 823
                                                                             --LeuAspPh
                                                                                                                                        AAAAGTTTKTGTGAAGATCTGACAGAGGGAAAGTTCTCATTTCCTACTATTCATGCTATT
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PRIOR FILING DATE: 2000-12-22
PRIOR PPLICATION NUMBER: 60,269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9542
LENGTH: 1284
                                                                      256 rLeuGlnAlaGluAlaValLysLysAspArg--
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Sequence 9542, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari L.
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949 ACAAGTCGCTTTCATTTTGTCATGTTGACAATGGATACGAAAGAGCCAGTTGCTTTGTCT 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 ValArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysPro 250
 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 ThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLysGlu 212
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                                                                                                                 GluAspilePheGln------GluGluPheSerThrProSerArgLys 115
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                                61
                                LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla
                                                                                               GlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAspGlu
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163 CCAGATTCGTGTTTATTCTTTTCAACTTTAGCGAAT
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\*

PIR\_73:\*

Database

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conserved hypothetical protein SPBC19G7.09 - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Dete: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999 C;Accession: T39840

RESULT 2

T39840

oligopeptide ABC t 90K protein - alfa transposase of IS1 hypothetical prote probable isolaucin transposase of IS1 DNA topoisomerase hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable 3-oxoacyl hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	LIGNMENTS  86K0919.1 - human n 11-Jun-1999 #text_change 13-Aug-1999 W.; Gassenhuber, J.; Wiemann, S. abase, March 1999 clone DKFZp586K0919	tch al Similarity 100.0%; Pred. No. 1.5e-130; 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0; LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 78 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117 LAPPDASILISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSI 117 LAPPDASILISNVCSIGDHVAQELFQGSSTPSRKGLVLQLIQSYQRANGANAVRGFR 138 LAPPDASILISNVCSIGDHVAQELFQGSSTPSRKGLVLQLIQSYQRANGANAVRGFR 137 LIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH
G72420 WMEM9 D86671 T02022 F86386 B81982 G86704 E97738 A84470 F83881 A42540 A43540 A13173 T30179 C96402 C96		Score 1667; Pred. No.  Mismatch ELFOGSDLGMAEE ELFOGSDLGMAEE FILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
пыпипипипипипипи	n DKFZ. Lrevis Gwes, Gwes, Gores D	18; 0.08; 0.08; 0.08; 1     1     0.08; 0.
625 790 790 543 1201 929 929 929 1475 445 1198 353 11175	protei s (man) equence ', D.; M in Sequ 6471 > BL:ALO5	y 1000 rvative VCSIGDHY VCSIGDHY IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
លេខកុខភេស្តេចក្រុមប្រភព ភេស្តុក្ខភេស្តិកក្រុមប្រភពក្រុម ភេសុក្ខកុខភេស្តិកក្រុមប្រភពក្រុម	hetical sapien 1999 #8 8759 Heubner e Frote e Frote 8759 : mRNA : mRNA ces: EM	tch 314; Conserv 314; Conserv LaPPDASILISNVC [
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0108480688844444	RESULT 1 T08759 conserved hypothetical protein DKFZp5 Conserved hypothetical protein DKFZp5 C;Species: Homo sapiens (man) C;Decies: 11-Jun-1999 #sequence_revisic C;Accession: T08759 R;Wambutt, R.; Heubner, D.; Mewes, H. Submitted to the Protein Sequence Data A;Reference number: 216471 A;Accession: T08759 A;McGoule type: mRNA A;Residues: 1-371 < www. A;Coss-references: EMBL:AL050283 A;Experimental source: adult uterus; C;Genetics: A;Note: DKFZp586K0919.1	Ouery Matches  Oy 19  Db 58  Oy 79  Db 118  Oy 139  Db 178  Oy 199  Db 238  Oy 259  Db 298  Oy 319

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312 ---- QDMPKLRRQIYKEL 325
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210 DVIKKDMPYFRLRTAKEI 227
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A;Molecule type: DNA
A;Residues: 1-662 <MIL>
A;Coss-references: EMBL:U23412; NID:9727446; PID:9727449; PIDN:AAA64293.1; CESP:T10F2...
A;Experimental source: strain Bristol N2
R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. submitted to the EMBL Data Library, February 1998
A; Reference number: 221884
A; Accession: T39840
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DMA
A; Residues: 1-568 < LYNN
A; Residues: 1-568 < LYNN
A; Residues: 1-568 < LYNN
A; Cross-references: EMBL:AL021839; PIDN:CAA17063.1; GSPDB:GN00067; SPDB:SPBC19G7.09
A; Experimental source: strain 972h-; cosmid c19G7
A; Genetics:
A; Genetics:
A; Genetics:
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A; Introns: 17/1; 51/1; 96/3; 197/3; 291/3; 342/3; 375/2; 619/2; 645/3; 649/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T10F2.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis
R; Miller, N.
Submitted to the EMBL Data Library, March 1995
A; Description: The sequence of C. elegans cosmid T10F2.
A; Reference number: Z18589
A; Accession: T16845
                                                                                                                                                                                                                                                                                                                                                                                       264 KKSPHDSTSRKASFRFVQSDQQPARNIVTSDIQNEKSLLLLIRD-LKEKQTESFQDWNEV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 VLTMDDLGTLYGQNWLNDQVMNMYGDLV----MDTVPEKVHFFNSFFYDKLRTKGYDGV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRWTK---NVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKL 317
                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFLQLKGLEISPPPTRPKFIPELEFPDNARKRALKYLNQSNSVSSSEPIITKFNIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 LISNVCSIG---DHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 ILSQINSLGIGSAYRGPQRYQNS----YQLSKQKEDKLLEEARIREGHRS------
                                                                                                                                                                                                                                                                                                                                                   EKAGQHSPLREEHVTCVQS-----ILDEFLQTYGSLIPLSTDEVVEKLEDIFQQ--
                                                                                                                                                                                                                                                                                                              59;
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                                                                                                                                                                                                                                                                    Length 568;
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                                                                                                                                                                                                                                                                                      Pred. No. 1.6e-18;
51; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.2%; Score 268.5; DB 2; Length (Best Local Similarity 26.4%; Pred. No. 3.3e-14; Matches 75; Conservative 53; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 QTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRM----
                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                    18.0%; Score 319.5; 28.7%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                           90; Conservative
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                                                                                                                                                                                                                                                                                      Similarity
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Best Local S
Matches 90
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hypothetical protein F6N23.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-oct-1999
C;Accession: T01233
R;Geisel, C
R;Geisel, C
R;Description: The sequence of A. thaliana F6N23.
A;Reference number: 214281
A;Reference number: 214281
A;Reference number: 214281
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N.Alternate names: hypothetical protein LPB11c
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Jaccesion: S63462
R.Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Submitted to the EMBL Data Library, September 1995
A; Reference number: S63462
A; Residues type: DNA
A; Cossion: S63462
A; Molecule type: DNA
A; Cossion: S63462
A; Molecule type: DNA
A; Cossion: S63462
A; Coss-references: EMBL: U36624; NID: g1276642; PID: g1039457; GSPDB: GN00016; MIPS: YPL0
C; Genetics:
A; Coss-references: SGD: S0005941
A; Map position: 16L
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173
                                                                                                                                                                                                                                                                                         98 SRWTTKRKLGYDLIDCDIIFVPIHIDIHWTLGVINNRERKFVYLDSLFT-----GAK 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Gaps
                                                                256 YLQAEAVKKDRLDFH-QGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQ---
                                                                                                                                                                                                                               -- DTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISVDV

    PGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVM-

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A;Map position: 5
A;Introns: 9/1; 21/2; 52/3; 85/3; 115/3; 147/3; 182/2; 213/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 RRRTITYFDSQRTLNRRCPKHIAKYLQAEAV--KKDRLDFHQGW 273
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Submitted to the EMBL Data Library, August 1997
A.Reference number: 221737
A.Accession: T37822
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-652 <DEV>
A.Residues: 1-652 <DEV>
A.Residues: 1-652 <DEV>
C.G.Sereferences: EMBL:298849; PIDN:CAB11507.1; GSPDB:GN00066; SPDB:SPAC17A5.07c
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                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable centromere protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T37822
                                                                                         |:: |: | | | | : :: | | : :: |: | | DYLNQKLKFDRSILEFEKDFKRYNEILNERKKIQEDLKKKKEQLAKK-----KLVP--- 405
                                                                                                                                                                                                           YGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTK----NVDIFN 210
                                                                                                                                                                                                                                 266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 K-----SYDGVKRWTKNVDIFNKELLLIPIHLEVHW------SLISVDVRRR--- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIVMSSVEQPSASKTRQAELTSNSPAILIFDSLANLHKGALNYLREYLLEEAFERKNVHL 537
                                                                                                                                         DEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTL 154
                                                                                                                                                                          406 -ELNEKDDDQVQKALA--SRENTQLMNRDNIE-------ITVRDFKTL 443
                                                                                                                                                                                                                                                                                                                                                                           LTMDDLGTLYGQNWLNDQVMNMY------GDLVMDTVPEKVHFFNSFFYDKLRT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| || | | ::| || ::| 363 ITNTDLTRLNEGEFLNDTIVDFYLRYLYCKLQTQNPSLANDT-----HIFNTFFYNRLTS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDF 269
                                    Gaps
                                                                   DHVAQEL-FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLST 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELLLIPIHL-EVHWSLISVDVRRRTITYFDS----QRTLNRRCPKHIAKYLQAEAVKKD
 Length 621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Match 12.6%; Score 222.5; DB 2;
Local Similarity 25.2%; Pred. No. 2e-10;
les 77; Conservative 56; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.6%; Score 205.5; DB 2 26.0%; Pred. No. 5.5e-09; tive 36; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 1
A;Introns: 2/2; 105/1; 387/2; 422/2; 501/2
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Best Local Similarity
Matches 60; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                         326 CHCKLT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLILT 617
Query Match
Best Local S
Matches 77
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hypothetical protein AT4g15880 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Accession: H85175
R; Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp Nature 402, 769-777, 1999
A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana. A; Reference number: A85001; MUID:20083488; PMID:10617198
A; Accession: H85175
A; Status: pre-liminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: Cress-references: GB:NC_001268; NID:97268336; PIDN:CAB78630.1; GSPDB:GN00140
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A Molecule type: DNA
A? Residues: 1-1034 <0DB>
A:Cross-references: GB:Z47047; EMBL:Z46861; NID:g603997; PID:g763315; MIPS:YIL031w
R;Melluh, P. B.; Koshland, D. E.
Submitted to the EMBL Data Library, May 1995
A;Reference number: S59668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMT4 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein Y19905.17; protein YIL031w
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 20-Feb-1995 #text_change 06-Feb-1998
C;Accession: S49947; S59668
R;Odell, C.; Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGQHSPLREEHVTCVQSILDBFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 LIQSYQRMPGNAMVRGFRVAYKRHVL------TMDDLGTLYGQNWLNDQVMNMYGD 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 IHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKD--RLDFHQGWKG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 GVTDVKKGENFRVEDTSMMLDSLSLDRDVDNDASSLEAYRKLMQS-----AEKRNSKLEA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVMDTVPE------KVHFFNSFFYDKL-RTKGYD--GVKRWTK----NVDIFNKELLLIP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 GTIWARRGAHLAPPDASILISNVCSIGD-----HVAQELFQGSDLGMAEEAERPGEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.1%; Score 12....
23.8%; Pred. No. 1.4e-08;
+ive 56; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: S59668
A, Molecule type: DNA
A, Residues: 1-49, DNA
A, Cross-references: EMBL:U27832; NID:9886765; PID:9886766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, December 1994
A;Reference number: $49931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: SGD:SMT4
A,Cross-references: SGD:S0001293; MIPS:YIL031w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: AT4g15880
A; Map position: 4
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Length 1034;

Score 196; DB 2;

11.18;

Query Match

RESULT 7 H85175

10;

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A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; C.; Chalwatzis, N.
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis t A; Reference number: A71400; MUID:98121113; PMID:9461215
A; Accession: E71424
A; Status: preliminary; nucleic acid sequence not shown; translation not.shown A; Molecule type: DNA
A; Residues: 1-398 < BEV>
A; Cross-references: GB:297339; NID:92244901; PID:92244945
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 21/3; 97/3; 123/1; 141/1; 212/2; 279/2; 298/1; 327/2; 407/2; 518/2; 626/2
A;Note: T16L1.110
        R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, Nature 391, 485-488, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.; Hoheisel, J.; Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T16L1.110 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Appr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
Cispecssion: T04979
R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Submitted to the Protein Sequence Database, November 1998
A;Reference number: Z15393
A;Accession: T04979
A;Accession: T04979
A;Molecule type: DNA
A;Residues: 1-710 <BEV>
A;Cross-references: EMBL:AL031394
A;Experimental source: cultivar Columbia; BAC clone T16L1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LIQSYQRMPGNAMVRGFRVAYKRHVL-----TMDDLGTLYGQNWLNDQVMNMYGD 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 LVMDTVPE-----KVHFFNSFFYDKL-RTKGYD--GVKRWTK----NVDIFNKELLLIP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 GTIWARRGAHLAPPDASILISNVCSIGD-----HVAQELFQGSDLGMAEEAERPGEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 190; DB 2; Length 39 ilarity 24.0%; Pred. No. 5.5e-08; Conservative 50; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 IHLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGREAYQKWTKNVDLFEKDYIFIDINCSFHWSLVII 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.2%; Score 163; DB 2; Lo
Best Local Similarity 31.7%; Pred. No. 2.1e-05;
Matches 32; Conservative 21; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T13D8.11 - Arabidopsis thaliana (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: O5-War-1999 #sequence_revision 05-War-1999 #text_change 22-Oct-1999 (5.5chartz, T02274 (5.7chantz, J.R.; Kwan, A.; Toriumi, M.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N absorription: Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.
A;Reference number: Z14649 A;Accession: T02274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:AC004473; NID:g3108025; PID:g3249071; GSPDB:GN00059; ATSP:T13D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Semecaro..
A/Sene: ATSP:T13D8.11
A/Map position: 1
A/Introns: 106/1; 1$4/3; 259/2; 275/3; 304/2; 332/2; 366/3; 399/2; 440/2; 478/3; 514/3
                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E71424
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03.4Mg-1998 #sequence_revision 03.4Mg-1998 #text_change 11.Jan-2002
C;Accession: E71424
                                                                                                                                                                                                                                                                                                                                            |:: | || || : | | : | : | : | : | : | | | SINNPLVNILTFDSLRQTHSREIDPIKEFLISYALDKYSIQLD---KTQIKMKTCPVPQQ 618
                                                                                                                                  442 YITINQDFKCLFNKDWVNDSILDFFTKFYIESSIEKSIIKREQVHLMSSFFYTKLISNPA 501
                                                                                                                                                                                                       ---SLI 227
                                                                                                                                                                                                                                                            561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 INVDEEEAQPSTVAEQAAELP--EGLIKLQL-------AIYK---LIVDK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 TCSLQEDICYPTRFLQQQISS-----SNQISADCHFFNTYFYKKLSDAVTYKGNDKDAF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 --GVKRWTKNVDIFNKELLLIPIHLEVHWSLISV-----DVRRRTITYFDSQRTLNRR- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 CPKHIAKYLQAEAVKKDRLDF-----HQGWKGYFK-----MNVARQNNDSDCGAFVL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 LGTL----YGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRT----KGYD---- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 LSTDEVVEKLEDIFQQEFSTPSRKGLV-LQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDD 150
                                                                                              HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEK-----VHFFNSFFYDKLRTKG-
                                                                                                                                                                                                                                                            DYYSNVKKWVNNTDLFSKKYVVIPINISYHWFSCIITNLDAILDFHQNKDKNDAINSDEI
                                                                                                                                                                                                                                                                                                                SVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN---VARQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 10.9%; Score 193; DB 2; Length 547.
I Similarity 25.9%; Pred. No. 4.7e-08;
67; Conservative 43; Mismatches 85; Indels
Pred. No. 6.2e-08;
                                                                                                                                                                                                       --YDGVKRWTKNVDIFNKELLLIPIHLEVHW------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 FFIKRFIEEAPORLKRKDL 512
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                27.28;
                                            52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNMSDCGVHVI 629
                                                                                                                                                                                                                                                                                                                                                                                                                       NNDSDCGAFVL 295
                Similarity
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A; Residues: 1-547 <VYS>
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Best Local Si
Matches 67;
                Best Local
Matches 5
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A;Cross-references: EMBL:U55855; PIDN:AAA98019.1; GSPDB:GN00020; CESP:Y38A8.3 A;Experimental source: strain Bristol N2; clone Y38A8 C;Genetics: A;Gene CESP:Y38A8.3 A;Gene CESP:Y38A8.3 A;Gene CESP:Y38A8.3 A;Map position: 2 A;Introns: 30/3; 58/3; 91/3; 182/3; 258/1; 288/2; 296/3; 339/3; 437/1; 505/3; 527/3;
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A; Experimental source: clone C41C4
C; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 2
A; Introns: 50/1; 110/3; 144/3; 327/3
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T19877
R;Burton, J.
Submitted to the EMBL Data Library, February 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 DEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 AYKRHVLTMDDLGTLYGQNWLNDQVMNMY-GDLVMDTVPE----KVHFFNSFFYD--KLR 192
                                                                                                                                                                                                                                                                             87 GSLIPLS-----TDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 DASILISNVCSIGDHVAQELFQGS---DLGMAEEAERPGEKAGQHSPLREEHVTCVQSIL 79
                                                                                                                                                                                                                                                                                                          566 V----VILVKDIKTLDRKEFLNDSVMAFMLNYIAFMLSSELMKSVHMCNTFLFVNLTRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 PPLCFSKRRPIEPEHIKIVKDNCPRVLRWTRKFDVLAKDYIIPINEDLHWLVIAVINPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 ------DVRRRT----ITYFDSQRTL----NRRCPKHIAKYLQAEAVKKDRLDFHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 DVSMREDDLFRMGSYNSOGYYADGTHLDGSIGEEDETSSGSNDOHMDFEEDDFDMESSMT
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                                                                                                                                                                                                                                                                                                                                                                            140 AYKRHVLTMDDLGTLYGQNWLNDQVM----NMYGDLVMDTVPEKVHFFNSFF---
                                                                                                                                                                         7.7%; Score 136; DB 2; Length 920; 22.8%; Pred. No. 0.005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | | : : | 337 GMKFASKNPTIYDEERVVVTRAENTPIQDNFYDCGLYVLHFIEGL 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 124.5; DB 2;
; Pred. No. 0.012;
64; Mismatches 138;
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A;Accession: T19877
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-342 <WIL>
                                                                                                                                                                                                                          36; Mismatches
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19.6%;
                                                                                                                                                                                                                            65; Conservative
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Best Local Similarity
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Rischulte, U.; Algn, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bubmitted to the Protein Sequence Database, April 2000
A; Reference number: 224541
A; Accession: T48800
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1240 <SCH>
A; Residues: 1-1240 <SCH>
A; Resperimental source: Cosmid contig 15E6; strain 74
C; Genetics: MCSP:15E6.80
A; Map position: 2
A; Introns: 8/3; 358/2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2650
R;Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A;Beference number: 220251
A;Reference number: 220251
A;Reference number: L20251
                                                                                                                        C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||: : : :::|:: ||
573 TSKVDLLSYDYIIVPVNEYYHWWVAIICNPGKLDPNHPRRSTNSSTSGTETSDSNSTESK 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633 SNGNIEKSDDVEMIDIDCEQARDQGQEIKAQEACGSVDRIETDSNEADSAGQDVVDLVAD 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 LISNVCSIGDHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 HQGWK--GYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFT----QQDMP 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.8%; Score 156; DB 2; L4 18.2%; Pred. No. 0.00016; Live 50; Mismatches 136;
                                                                               - Neurospora crassa
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                                                                             SMT4 related protein [imported] - N
N;Alternate names: protein 15E6.80
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Matches 86; Conservative
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A;Cross-references: EMBL:AF043699; PIDN:AAB97567.1; GSPDB:GN00019; CESP:K02F2.4
A;Experimental source: strain Bristol N2; clone K02F2
C;Genetics:
A;Gene: CESP:K02F2.4
A;Map position: 1
A;Introns: 16/3; 72/2; 103/3; 139/2; 203/2; 238/2; 273/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K02F2.4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T32915
R;Maggi, L.; Goela, D.
R;Maggi, L.; Goela, D.
R;Maggi, L.; Goela, D.
R;Maggi, L.; Goela, D.
R;Maggi, L.; Goela, D.
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R;Maggi, L.; Goela, D.
R;Maggi, L.; Goela, D.
R;Marcallamiary; translated from GB/EMBL/DDBJ
A;Residues; 1-311 < MAGS.
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A;Residues; 1-311 
247 AQARTV-IFDSQLTADLNNLQNMATLI--ESFWKYSYEKRTGNAMPFPLPCILPQRMPQQ 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 FYDKLRT--------KGYDGVKRWTKNVDIF-NKELLLIPIHLE--VHWSLI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 SV------DVRRRTITYFDSQRTLNRR-----CPK------251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----HIAKYLQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 RRHIIP-----PLFHNGWVGRNEDRTLLNDTIIEFYMCDWMRLEVFDEATRASSHVFHSF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.7%; Score 118.5; DB 2; Length 3
Best Local Similarity 19.8%; Pred. No. 0.034;
Matches 51; Conservative 35; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: December 16, 2002, 20:15:46 Job time: 259 secs
                                                                                                                                                  285 NNDSDCGAFVLQYCKHLALSQP 306
                                                                                                                                                                                                                   :: :: | :|
263 EYFT---KYNTAWQSLP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 KHLALSQPFSFTQQDMP 315
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
T32915
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us-09-848-852a-3.rsp

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GenCore version 5.1.3
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OM protein - protein search, using sw model

December 16, 2002, 19:28:45; Search time 207 Seconds (without alignments) 66.522 Million cell updates/sec Run on:

US-09-848-852A-3 1772 1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	schizosa	Q09353 caenorhabdi	Q02724 saccharomyc	013769 schizosacch	P40537 saccharomyc	рошо	homod	Q09275 caenorhabdi	_		-		-		033102 mycobacteri	-		-		Q13099 homo sapten		m ger		_	P31956 arthrobacte	Q97wh0 sulfolobus	P06700 saccharomyc	P46208 bacillus su	P39531 saccharomyc	Q47013 escherichia	P11913 neurospora	Q13823 homo sapien	Q57662 methanococc
SUMMARIES	ID	LP1	YRW3_CAEEL	ULP1_YEAST	- 1	ULP2_YEAST	SUS2_HUMAN	SUS1_HUMAN	YQG6_CAEEL	YZ28_METJA	V90K_AMVLE	VPRT_ASFB7	YR22_CAEEL	HTPG_CAMJE	VPRT_ASFM2	DNLJ_MYCLE	FER1_CAEEL	DYHC_EMENI	HUGA_APIME	RP54_BRAJA	TG37_HUMAN	Z155_HUMAN	GGPP_MOUSE	HTPG_FUSNN	RN5A_MOUSE	PAC_ARTVI	RA50_SULSO	SIR2_YEAST	HTPG_BACSU	YJU4_YEAST	ELAD_ECOLI	MPPB_NEUCR	NGP1_HUMAN	Y209_METJA
	DB	П	П	æ	Н	-	٦	ŋ	7	٦	П	٦	7	Н	Н	-1	7	н	Н	H	Н		Н	Н	Н	Н	Н	Н	Н	-	7	П	1	1
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dР	Query	18.	S	2	11.6	_	9.6	8.1	7.0	6.0	5.5	5.2	5,1	5.0			4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.7	4.7	4.7	4.7
	Score	O,	268.5	222.5	205.5	196	170.5	143	124.5	105	6	92.5	06	83	87.5	87.5	87.5	87.5	86.5	86.5	98	85.5	82	82	82	82	82	84.5	84.5	84.5	84	84	œ	83.5
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P56966 b geranylge P34036 dictyosteli	058600 methanococc 09vul9 drosophila	7 01	0, 14	Q05490 pseudomonas P09959 saccharomyc	095749 h geranylge
GGPP_BOVIN DYHC_DICDI	MT52_METJA FUTA_DROME	KADS_SCRFO YFJD_HAEIN YLD8_STRCO	RSC4_YEAST TOP2_PENCH	LICH_PSEGL SWI6_YEAST	GGPP_HUMAN
н н					<b>-</b>
294	366	4 20 4 59	625 1587	353 803	300
4.7	7.4	, 4 4 , 7 . 7	4.7	4 <b>4</b> .6	4.6
83.5	8880	82.5 82.5	82.5 82.5	85 87	81.5
34 35	37	0 8 4 0 0 0	<b>4</b> 1	<b>4</b> 3	45

## ALIGNMENTS

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SEQUENCE
                                                                                                                                               Match
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                     323 DFLQLKGLEISPPPTRPKFIPELEFPDNARKRALKYLNOSNSVSSSEPIITKFNIP---- 378
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        59 EKAGQHSPLREEHVTCVQS-----ILDEFLQTYGSLIPLSTDEVVEKLEDIFQQ---- 107
                                                                                                                                                                                                                                              -----EFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRH 144
                                                                                                                                                                                                                                                                                      145 VLTMDDLGTLYGQNWLNDQVMNMYGDLV----MDTVPEKVHFFNSFFYDKLRTKGYDGV 199
                                                                                                                                                                                                                                                                                                                               200 KRWTK--NVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSORTLNRRCPKHIAKYL 257
                                                                                                                                                                                                                                                                                                                                                                     258 QAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKL 317
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                     59;
                                                                                                                                                                 DB 1; Length 568;
                                                                                                                                                               18.0%; Score 319.5; DB 1; Length 28.7%; Pred. No. 2.2e-18; tive 51; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubmitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases.
 Usage by
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AAF9771440302D9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein T10P2.3 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     659 AA.
modified and this statement is not removed.
                                                                    InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSTIE; PS50600; ULP_PROTEASE; 1.
Hydrolase; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                        EMBL; AL021839; CAA17063.1; -.
                                                                                                                                           64940 MW;
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                               463
                                                                                                                                                                                                                                                                                                                                                                                                              318 R----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                  555 RIKMAASIIDAQIY 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miller N.;
Submitted (MAR-1995)
                                                                                                                       480 4
527 5
568 AA;
                                                   Q02724; 1EUV.
                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                            MEROPS; C48.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (MA)
                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRW3_CAEEL
Q09353:
                                                                                                                        ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS
                                                                                                                                                                Query Match
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                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r10F2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
YRW3_CAEEL
                                                                                                                                                                                                                                               108
                                                                                                                                                                                    Matches
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                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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KR MEDLINE=9731371; PubMed=9169875;

Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Bussey H., Storms R.K., Ahmed A., Albermann K., Benes V., Araujo R., Aparicio A., Barchal B.G., Badcock K., Benes V., Araujo R., Aparicio A., Bruckner M., Carpenter J., Cherry J.M., Andong E., Davis R.W., Coster F., Davis R.W., Dietrich F.S., Delius H., Dipaloalo T., Dubois E., Duesterhoeft A., Dietrich F.S., Delius H., Dipaloalo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Andrews-Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Amarche R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D., Ameller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scharfe M., Schramm S., Schreder M., Sdicu A.M., Tettellin H., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wanbutt R., Walsh S.V., Walsh S.V., Wanbutt R., Walsh S., Walsh S.V., Walsh S.V., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., Walsh S., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 ILSQINSLGIGSAYRGPQRYQNS----YQLSKQKEDKLLEEARIREGHRS------ 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DIVPEKVHFFNSFFYDKLRIKGYDGVKRWIKNVDIFNKELLLIPIHLEVHWSLISVDV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 NGDSKYPKIYAFNTFFYSNIVSKGYASVKRWTRKVDIFAFDIVLVPVHLGMHWCMAVIDM 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LISNVCSIG---DHVAQELFQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTRG------DRLEDV-----RKRLELQGIAIRPKVEKKKVDDFMALPDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 QTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRM----
ρλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75304 MW; 4F66F0082D470EB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  594 GEKKIEFYDSLYDGNTAVLPALRGYLEAESLDKKKTAMNF-SGW 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRIITYFDSQRILNRRCPKHIAKYLQAEAV--KKDRLDFHQGW 273
     Usage
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15-UN-2002 (Rel. 41, Last annotation update)
Ubiquitin-like-specific protease 1 (EC 3.4.22.-).
ULPI OR YPL020C OR LPB11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.2%; Score 268.5; DB 1; 26.4%; Pred. No. 3.6e-14; iive 53; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ž
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                                                                                                                                                                                                                                                                           MEROPS, C48.002; ...
WormPep; T10F2.3; CE26951.
InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                          EMBL; U23412; AAK21468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 26.48
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 protein.
659 AA; 7
                                                                                                                                                                                                                                             002724; 1EUV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULP1_YEAST
Q02724;
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Matches
               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMB. outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                      Mol. Ceil 5:865-876(2000).

-!- FUNCTION: Protease that catalyzes two essential functions in the SUMO pathway: processing of full-length SWT3 to its mature form and deconjugation of SWT3 from targeted proteins. Has an essential role in the G2/M phase of the cell cycle.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                               X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 401-621 IN COMPLEX WITH SMT3. MEDLINE-20337970; Pubmed=10882122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 DEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 -ELNEKDDDQVQKALA-|-SRENTQLMNRDNIE---------ITVRDFKTL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 YGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTK----NVDIFN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 KELLLIPIHL-EVHWSLISVDVRRRTITYFDS----QRTLNRRCPKHIAKYLQAEAVKKD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 RLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKEL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 DYLNQKLKFDRSILEFEKDFKRYNEILNERKKIQEDLKKKKEQLAKK-----KLVP--- 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 DHVAQEL-FQGSDLGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLST 94
                                                                                                                                   "Ulp1-SUMO crystal structure and genetic analysis reveal conserved interactions and a regulatory element essential for cell growth in
                                                                                                                                                                                                                                                                                                                                                                                                SGD; S0005941; ULP1.
InterPro; IPR003653; SUMO_protease.
Jefam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
Hydrolase; Thiol protease; Ubl conjugation pathway; 3D-structure.
                                               Li S.J., Hochstrasser M.;
"A new protease required for cell-cycle progression in yeast.";
Nature 398:246-251(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72377 MW; F71132817FAF0B41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 12.6%; Score 222.5; DB 1; Similarity 25.2%; Pred. No. 1.8e-10; 77; Conservative 56; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASE
                                  MEDLINE=99191836; PubMed=10094048;
                                                                                                                                                                                                                                                                                                                                                            EMBL; U36624; AAB68167.1; -. PDB; 1EUV; 07-JUN-00.
                                                                                                                        Mossessova E., Lima C.D.;
Nature 387:103-105(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            621 AA;
                                                                                                                                                                                                                                                                                                                                                                                     MEROPS; C48.001; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   531
580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAGANNE-2188401; PubMed=11859360;
RAGANNE-2188401; PubMed=11859360;
RAGANNE-2188401; PubMed=11859360;
RAGOUTOS V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RAGOUTOS V., Peat N., Hayles J., Basham D., Bowman S.,
Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Ragnels S., Goble A., Hamlin N., Harris D., Hidalyo J., Hodgson G.,
RAGONG P., Woule S., Mungall K., Murphy L., Niblett D., Odell C.,
RAGONG P., Noule S., Mungall K., Murphy L., Niblett D., Odell C.,
RAGONG P., Noule S., Mungall K., Murphy L., Sharp S.,
RAGITON J., Simmond M., Squares R., Squares S., Stevens K.,
Ragelton J., Simmond M., Squares R., Squares S., Stevens K.,
RAGONG K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RAGONG K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RAGONG K., Taylor R.G., Tivey A., Walsh S.V., Grymonprez B.,
RAGONG K., Taylor R.G., Lehrach H., Reinhardt R., Pohl T.M.,
RAGONG W., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RAGONG W., Cuzado L., Jimenez J., Sanchez M., Galzon A., Thode G.,
RAGONG W., Cuzado L., Jimenez J., Sanchez M., Galzon R., Porsburg S.L.,
RAGONG W., Corombie W.R., Paulsen I., Potashkin J.,
RY Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RY The genome sequence of Schizosaccharomyces pombe.";
RY Nature 415:871-880(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                  Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the SWISS-PROT data bank.
                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ubiquitin-like-specific protease 2 (EC 3.4.22.-).
ULP2 OR SPACI7A5.07C.
652 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY
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InterPro; IPR003653; SUMO_protease.
Pfam. PF02902; Peptidase_C48; 1.
PROSTIE; PS50600; UIP_PROTEASE; 1.
Hydrolase; Thiol protease.
                                                                         16-OCT-2001 (Rel. 40, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896
   SCHPO
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SEQUENCE
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Hydrolase; Thiol protease; Ubl conjugation pathway.
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              196
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                                     478 EIVMSSVEQPSASKTRQAELTSNSPAILIFDSLANLHKGALNYLREYLLEEAFERKNVHL 537
363 ITNTDLTRLNEGEFLNDTIVDFYLRYLYCKLQTQNPSLANDT-----HIFNTFFYNRLTS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 HVLTMDDLGTLYGQNWLNDQVWNMYGDLVMDTVPEK -----VHFFNSFFYDKLRTKG- 195
                        194 K-----GYDGVKRWTKNVDIFNKELLLIPIHLEVHW------SLISVDVRRR---
                                                                        ----TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BENOMYL SENSITIVITY; HIGH COPY SUPPRESSOR OF A TEMPERATURE SENSITIVE MUTATION IN MIF2.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycoties;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser P. Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Mhitchead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                         270 HQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPK-LRR 319
                                                                                                                                                538 KSTDIRGFHAKVPQQSNFSDCGIYALHFVE-LFLETPEQVIANTLDKSLRR 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan: PP02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
Hydrolase; Thol protease.
SEQUENCE 1034 AA; 116882 MW; 782789B3B1DC37F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ubjquitin-like-specific protease 2 (EC 3.4.22.-).
ULP2 OR SWT4 OR YIL031W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 196; DB 1;
Pred. No. 4.7e-08;
                                                                                                                                                                                                              PRT; 1034 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
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27.2%;
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Meluh P.B., Koshland D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C48.005; -.
SGD; S0001293; ULP2.
InterPro; IPR003653;
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                                                                                                                                                                                                             ULP2_YEAST
P40537;
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ULP2_YEAST
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                                                                                                                                                                                                                         618
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUS2_HUWAN STANDARD; PRT; 984 AA.
Q9BQF6; Q9C0F6; Q9HBT5;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
SUMO-1-specific protease 2 (EC 3.4.22.-) (Sentrin-specific protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O., "Prediction of the coding sequences of unidentified human genes. XI) The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
                                                                                                                                                                                             SVDVRRRTITYFDSQRTLNRRCPKH1AKYLQAEAVKKDRLDFHQGWKGYFKMN---VARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain; MEDILME-21154917; PubMed=11230166; MEDILME-21154917; PubMed=11230166; Miemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Dueskerhoeft A., Rehrer K., Strack N., Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Riein M., Poustka A.; Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gong L., Yeh E.T.;
"SENP7, a novel human sentrin-specific protease.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
--YDGVKRWTKNVDIFNKELLLIPIHLEVHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL136599; CAB66534.1; -. EMBL; AB051494; BAB21798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF217504; AAG09703.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 229-984 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 747-984 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 7:347-355(2000).
                                                                                                                                                                                                                                                                                                                                                                        619 PNMSDCGVHVI 629
                                                                                                                                                                                                                                                                                                  285 NNDSDCGAFVL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUSP2 OR KIAA1707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C48.009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
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us-09-848-852a-3.rsp

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11;
            BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

R -> K (IN REF. 2).

Q -> H (IN REF. 2).

TRKENNLTEDNPALS -> MKKFLYIKSVFHTLR (IN REF. 3).

N -> S (IN REF. 1).

Q -> R (IN REF. 1).

Q -> R (IN REF. 1).

MW; 317E8B7B4128EDID CRC64;
                                                                                                                                                                                                                                                      756 DNPNLSMAQRRHKRVRTWTRHINIFNKDYIEVPVNESSHWYLAVICFPWLEEAVYEDFPO 815
                                                                                                                                                                                                                                                                                                                                                                                     816 TVSQQSQAQQSQNDNKTIDNDLRTTSTLSLSAEDSQSTESNMSVPKKMCKRPCILILDSL 875
                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LTMDDLGTLYGQNWLNDQVMNMYGDLVM-----DTVPEKVHFFNSFFYDKLRTK----- 194
                                                                                                                                                                                                                                                                                                                                                                                                                    ------YLQAEAVKKDRLDFHQGWKGYFKMN-----VARQNNDSDCGAFV 294
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
MEDLINE-20261527; PubMed-10799485;
MEDLINE-20261527; PubMed-10799485;
Kim K.I., Baek S.H., Jeon Y.-J., Nishimori S., Suzuki T., Uchida S., Shimbara N., Saitoh H., Tanaka K., Chung C.H.;
"A new SUMO-1-specific protease, SUSP1, that is highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGGZRI; 09UJVS; 094891;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SUMO-1-specific protease 1 (EC 3.4.22.-) (Sentrin-specific protease
SENP6) (Protease FKSG6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang Y.-G.; "Identification of FKSG6, a novel protein with protease activity."; submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                        ------ISVDVRRR---TITYFDSQRT-LNRRCPKHIAK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          Indels 111;
                                                                                                                                                                            DB 1; Length 984;
                                                                                                                                                                                                                                                                                                ------GYDGVKRWTKNVDIFNKELLLIPIHLEVHWSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeh E.T., Gong L., Kamitani T.; "Ubiquitin-like proteins: new wines in new bottles."; Gene 248:1-14(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQYVESFFKDPIVNF---ELPIHLEKWFPRHVIKTKREDIREL 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQYCKHLALSQPFSFTQQDMP------KLRRQIYKEL 325
                                                                                                                                                                                                       41; Mismatches 67;
                                                                                                                                                                           9.6%; Score 170.5; DB 1
22.6%; Pred. No. 5.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND CHARACTERIZATION.
 PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 275:14102-14106(2000)
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MEDLINE=20267842; PubMed=10806345;
                                                                                                                                               112264 MW;
                                                                                                                                                                         Query Match
Best Local Similarity 22.6*
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reproductive organs."
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                                                                                                                  828
881
984 AA;
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          ACT_SITE
ACT_SITE
CONFLICT
CONFLICT
CONFLICT
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 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠;
ش
                                                                                                                                                                          -!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Highly expressed in reproductive organs, such as testis, ovary, and prostate.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| :|| | :|| :|| :|| ||: : : ::| |:|||| :|
668 VINEDLHCLNEGEFLNDVIIDFYLKYLVLEKLKKEDADRIHIFSSFFYKRLNQRERRNHE 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                            Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Fotani H., Nomura N., Ohara O.; The conjusting sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; In vitro."; Pub. Res. 5:277-28(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.1%; Score 143; DB 1; Length 1112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 LIMDDLGTLYGQNWLNDQVMNMY-GDLVMDTV----PEKVHFFNSFFYDKL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           765 765 BY SIMILARITY.
917 BY SIMILARITY.
120 1030 BY SIMILARITY.
121 121 T -> M (IN REF. 1 AND 4).
1043 1043 Q -> E (IN REF. 1 AND 4).
1105 1106 Y -> C (IN REF. 1 AND 4).
1112 AA; 126144 MW; B6E53875C3833A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 35.7 kDa protein C41C4.6 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 -----RTKGYDGVKRWTKNVDIFNKELLLIPIHLEVHWSLISV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiol protease; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                MEDLINE-99087487; Pubmed-9872452;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF196304; AAF04852.1; -. EMBL, AF307849; AAG29831.1; -. EMBL, AF306508; AAG30253.1; -. EMBL, AB018340; BA34517.1; -. MEROPS; C48.004; --
SEQUENCE OF 29-1112 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%;
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765
917
1030
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Burton J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQG6_CAEEL
Q09275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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δλ
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Best Local Similarity 20.5
Matches 52; Conservative
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P03593;
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                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                       80 DEFLQTYGSLIPLSTDEVVEKLEDIFQQEFSTPSRKGLVLQLIQSYQRMPGNAMVRGFRV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                   ED-----LVDEDEEEEDEEDNDEWTNQKRTDNQNS-----VAYYAAM---EMLR-IRF 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 AYKRHVLTMDDLGTLYGQNWLNDQVMNMY-GDLVMDTVPE----KVHFFNSFFYD--KLR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-96337999; Pubmed-8688087;

MEDLINE-96337999; Pubmed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 AQARTV-IFDSQLTADLNNLQNMATLI--ESFMKYSYEKRTGNAMPFPLPCILPQRMPQQ 303
                                                                                                                                                                                                                                                                                                                                               DASILISNVCSIGDHVAQELFQGS---DLGMAEEAERPGEKAGQHSPLREEHVTCVQSIL 79
                                                                                                                                                                                                                                                                                                                                                                            23 DVSMREDDLFRMGSYNSQGYYADGTHLDGSIGEEDETSSGSNDQHMDFEEDDFDMESSMT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VKRWTKNVDIFNKELLLIPIHLEVHWSLISV----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 VRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKM-----NVARQ
                                                                                                                                                                                                                                                                                                                    57;
                                                                                                                                                                                                                                                                                        7.0%; Score 124.5; DB 1; Length 342; 9.6%; Pred. No. 0.007; ve 64; Mismatches 138; Indels 57
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                            PROSITE; PS50600; ULP_PROTESSE; 1.
Hypothetical protein; Hydrolase; Thiol protease.
SEQUENCE 342 AA; 39503 MW; 80ABF2AECCAECAD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJECL28.
Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanocaldococcaceae; Methanocaldococcus
                                                                                                                                                                                                 InterPro, IPR003653; SUM_protease.
Pfam; PF02902; Peptidase_C48; 1.
PROSITE; PS50600; ULP_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNDSDCGAFVLQYCKHLALSQP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 TNNFDCGIFIAEFARRFLLSPP 325
                                                                                                                                                           EMBL; Z48045; CAA88104.1; -.
                                                                                                                                                                                                                                                                                                     Similarity 19.6%;
                                                                                                                                                                         MEROPS; C48.UPW; -..
WormPep; C41C4.6; CE01521
                                                                                                                                                                                                                                                                                                                    63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 TKGYDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YZ28_METJA
Q60287;
                                                                                                                                                                                                                                                                             Query Mar.
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Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 --IQVANEEDILLAID-EAHDLVIQKEFRKRAITGVKKCIDRAGGCVLLTATPELINLNN 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 HVLTMDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alfalfa mosaic virus (strain 425 / isolate Leiden).
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornelissen B.J.C., Brederode F.T., Veeneman G.H., van Boom J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of alfalfa mosaic virus RNA 2.";
Nucleic Acids Res. 11:3019-3025(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 105; DB 1; Length 1272; Best Local Similarity 25.9%; Pred. No. 1.4; Matches 42; Conservativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.5%; Score 97; DB 1; Length 790; 20.5%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
SEQUENCE 1272 AA; 149438 MW; 88E7AE8C48629DEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pfam; PF00978; RNA_dep_RNApol2; 1.
SEQUENCE 790 AA; 89855 MW; B435C9EB9AA853C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 KNVDIFNKELLIPIHLEVHWSLISVDVRRRTIT--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 -----YFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83220723; PubMed=6304618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
                                                                                                        Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L77118; AAC37099.1; -. TIGR; MJECL28; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X01572; CAA25728.1; -. EMBL; K02702; AAA46290.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92263807; PubMed=1316688;
Garcia-Beato R., Freije J.M., Lopez-Otin C., Blasco R., Vinuela E.;
"A gene homologous to topoisomerase II in African swine fever virus.";
Virology 188:938-947(1992).
                           --PSRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYG 169
                                                                           353 ALSTRKGTQTEAL------LAIKKRNMNVPNLGQIYDVNSVANSVVNKLL 396
                                                                                                                                     397 TTVID--PDKLCMFPDFISEGEVSYFQDYIVGKNPDPELYSDPLGVRSIDSYKHMIKSV- 453
                                                                                                                                                                                      -----LKPVEDNSLHLE------RPMPATITYHDKDIVMS-SSPIFLAAAARLMLI 497
                                                                                                              DLVMDTVPEKVHFFNSF---------FYDKLRTKGYDGVKRWTKNVD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yanez R_1J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.; "Analysis of the complete nucleotide sequence of African swine fever
          ---IPLSTDEVVEKLEDIFQQEFST-
                                                                                                                                                             208 IFNKELLLIPI-----HLEVHWSLISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION, CHARACTERIZATION, AND MUTAGENESIS.
MEDLINE-20576431; PubMed-11031264;
Andres G., Alejo A., Simon Wateo C., Salas M.L.;
Affrican swine fever virus protease, a new viral member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMO-1-specific protease family.";
J. Biol. Chem. 276:780-787(2001).
-!- FUNCTION: Protease involved in the processing of the virus
                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyproteins.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C48.
                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Polyprotein processing peptidase (EC 3.4.22.-).
                                                                                                                                                                                                                                                                                                                                                                                               African swine fever virus (strain BA71V) (ASFV)
                                                                                                                                                                                                                                                                                                        273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A42549; A42549.
MEROPS; C48.050; -.
Hydrolase; Thiol protease; Late protein.
ACT_SITE 168 PROBABLE.
                                                                                                                                                                                                                                                                                                        PRT;
           VQSILDEFLQTYGSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M88699; AAA42734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 208:249-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18466; AAA65340.1;
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                 263 KKDRL----DFHQ 271
                                                                                                                                                                                                                                         498 LRDKITIPSGKFHQ 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10498;
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                                                                                                                                                                                                                                                                                                       VPRT_ASFB7
                                                                                                                                                                                                                                                                              RESULT 11
VPRT_ASFB7
         75
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                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                       168 HWVAIFVDMRGDCWSIEYFNS---AGNSPPGPVIRWM--ERVKQQLLKIHHTVKTLAVIN 222
                                                                                                                                                                                                                                             223 HWSLISVDVRRR--TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN 280
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
GPRK SUBFAMILY.
--- SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last annotation update)
Putative G protein-coupled receptor kinase W02B3.2 (EC 2.7.1.-).
                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                          281 VARQNNDSDCGAFVLQYCK-----HLALSQPFSFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                      Length 273;
                                                                                                                                                                                              44; Indels
                                               H->R: LOSS OF ACTIVITY.
C->S: LOSS OF ACTIVITY.
C5AA778179C57C17 CRC64;
                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                727 AA
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InterPro; IPRO00361; Pkinase_C
InterPro; IPR000342; Regl_Gprotein.
InterPro; IPR000342; Regl_Gprotein.
InterPro; IPR000342; Regl_Gprotein.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00717; GPCEKINASE.
ProDom; PD000001; Euk_pkinase; 1.
PRINTS; SM00233; PR; 1.
SMART; SM00315; RGS; 1.
SMART; SM00133; STKC; 1.
SMART; SM00130; STKC; 1.
PR0SITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                 Score 92.5; D
Pred. No. 2.1;
                                                                                                                                                                                              20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
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     POTENTIAL.
                              PROBABLE
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000239; GPCR_kinase.
187
232
168
232
31550 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                              5.2%;
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HSSP; P25098; 1BAK.
                                                                                                                                                                                                29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                 273 AA;
                                                                                                                                                 Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
STRAIN-Bristol N2;
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  187
232
168
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Q09639;
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  ACT_SITE
ACT_SITE
MUTAGEN
MUTAGEN
SEQUENCE
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                                                                                                                    15;
                                                                                                                                                                                          EF-----STPSRKGLVLQLIQSYQRM--PGNAMVRGFRVAYKRHVLTMDDLG 152
                                                                                                                                                                                                         : : : | | :: :: | 62 KLGFLLLKDYAENVSESPCPQIKFYEAIKEYEKMETPDERLTKA-REIYDHHIM-VEMLA 119
                                                                                                                                                                                                                                                       212 ELLIPIHLEVHWSLISVDVRRRTITYFDSQRTLNR-----RCPK-HIAKYLQAEAVK 263
                                                                                                                                                                                                                                                                                                                                      -----HNVARQNNDSDCGAFVLQYCK----H 300
                                                                                                                                           LGMAEEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVEKLEDIFQQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIARE 20150912; pubmed=10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M., Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chaperone protein htpG (Heat shock protein htpG) (High temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                      165 FLESDKFTRFCQWKNLELNM-QLTMNDFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLD
                                                                                                                                                                   15 MAMEKSRSQPAARASKRIVLPD---PSVRSIMQKFLEKSGDM------KFDKIFNQ
                                                                                                                                                                                                                                        153 TLYGQNWLNDQVWNWYGDLVMDTV-PEKVHFFNSFFYDKLRTKGYDGVKRWTKNVDIFNK
                                                                                                                                                                                                                                                                                                                                                           224 KKRIKMKQGETLALNEHIMLSLVSTGQDCPFIVCMTYAFQSPDKLC--FILDLMNGGDLH
                                                                                                                    80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
                                                                                             DB 1; Length 727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Molecular chaperone. Has ATPase activity (By
                                                                                                        ; Pred. No. 11;
50; Mismatches 122; Indels
                                                         Y SİMILARITY.
AA0530D8A9DA57D7 CRC64;
                                              SIMILARITY).
                                  (BY SIMILARITY)
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      608 AA.
                                                                                            5.1%; Score 90; 19.7%; Pred. No. 1
             C-TERMINAL.
                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                 ATP ATP
                                                                   83361 MW;
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                455
700
175
205
220
                                                                                                                                                                                                                                                                                                                                    264 KDRLDFHQGWKGYFK--j-
                                                                                                                                                                                                                                                                                                                                                                                    301 LALSQPFSFTQQDM 314
191
456
54
197
220
318
                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein G).
HTPG OR CJ0518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter
                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTPG_CAMJE
Q9PHZ3;
                                                         ACT_SITE
SEQUENCE
                                                                                             Query Match
Best Local
                                 NP_BIND
BINDING
           DOMAIN
DOMAIN
                                                                                                                  Matches
SELLE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
and for commercial
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                       (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 REEHVTCVQSIL--DEFLQTYGSLIPLSTDEVVEKLEDIFQ-----QEFSTPSRKG-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 ---LVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYGQNWLNDQVMNMYGDLVM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 ISVDVRRRTITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMNVAR--- 283
                                                                                                                                                   213 EGKTELKISQINK---ANALWR-----MQKSSLKAEDYERFYEQNFHDSNKPLLY---L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 IDVE------DLPLN-----VSREILQENQILKGIKEASVKILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 DIVPEKVHFFNSFF-----YDKLRIKGYDGVKRWIKNVDIFNKELLLIPIHLEVHWSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S., Bristow C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome of a pathogenic African swine fever virus isolate (Malawi LIL20/1).",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 ----QNNDSDCGAFVLQYCKHLALSQPF-----SFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 ELEKLKNNDKE------KYLSFFKTFGKVLKEGLYGFGGEKDSLLKLMLYK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94292916; PubMed-8021596;
Dixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow
Hammond J.M., Smith G.L.,
"Nucleotide sequence of a 55 kbp region from the right end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        African swine fever virus (isolate Malawi Lil 20/1) (ASFV).
Viruses; dsDNA viruses, no RNA stage; Asfarviridae; Asfivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Gen. Virol. 7:1655-1684(1994).
-!- FUNCTION: Protease involved in the processing of the properties (By similarity).
-!- SUBCELLOGATION: Cytoplasmic (By similarity).
-!- SUBCELLOGATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polyprotein processing peptidase (EC 3.4.22.-). ORFIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Pred. No. 11; ive 45; Mismatches
                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0%; Score 89;
                         entities requires a license agreement
                                                                                                                         HSSP; P02829; 1AH8.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR001404; Hsp90.
                                                                                            EMBL; AL139075; CAB75155.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 21.13
nes 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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VPRT_ASFM2
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Matches
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us-09-848-852a-3.rsp

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                                                                                                                                                                                                                                                                                                                                                   5;
use by non-profit institutions as long as its content is in no way madified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 HWVAIFVDMRGDCWSIEYFNS---AGNSPPGPVIRWM--ERVKQQLLKIHHTVKTLAVTN 222
                                                                                                                                                                                                                                                                                                                                                                                                223 HWSLISVDVRRR--TITYFDSQRTLNRRCPKHIAKYLQAEAVKKDRLDFHQGWKGYFKMN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.NCBL_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MXY-2000 (Rel. 39, Created)
30-MXY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD+]).
LIGA OR LIG OR ML1705 OR MLCB637.10.
                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY! BELONGS TO THE NAD-DEPENDENT DNA LIGASE FAMILY. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 VARQNNDSDCGAFVLQYCK-----HLALSQPFSFTQQDMPKLRRQIYK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 IRHQRSQTECGPYSLFYIRARLDNVSYTHFISTR---ITDENMYKFRTHLFR 271
                                                                                                                                                                                                                                                                                                4.9%; Score 87.5; DB 1; Length 273; 25.0%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                          D6AD6DAC62C25F3B CRC64;
                                                                                                                                                     ACT_SITE 187 BY SIMILARITY.

ACT_SITE 187 BY SIMILARITY.

ACT_SITE 232 232 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                              21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deoxyribonucleotide (N+M).
                                                                                                                                                                                                                                                       31493 MW;
                                                                                                                 EMBL; X71982; CAA50819.1; -.
                                                                                                                                                                                                                                                                                                                        Best Local Similarity 25.03
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                               232 2
273 AA;
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                                                                                                                                                                                 ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
DNLJ_MYCLE
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569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 -LRDGSEREFVMPTTCPECGTTLAPEKEGDADIRCPNARSCPGQLRERVFHVA-SRSALD 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 MDDLGTLYGQNWLNDQVMNMYGDLVMDTVPEKVHFFNSFFYDKLRTKGYDGVKRWTKNVD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 GSDLGMA-----EEAERPGEKAGQHSPLREEHVTCVQSILDEFLQTYGSLIPLSTDEVVE 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 IFNKELLLIPIHLEVHWS-LISVDVR-----RRTITYFDSQRTLNRRCPKHIAKY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 ----KAKTAPL----WRVLVALSIRHVGPTAARALATEFGSVDAILAASPEQLAAVEGV
                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%; Score 87.5; DB 1; Length 694;
83.1%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | : | : | : | : | : | : | : | 570 GTTIAAAVTEWFTVDWHRVIVNKWRAAGVRMYDERDTS--VLPTCEGLTI 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---LQAEAVKKDRLDFHQGWKGYFKMNVARQNNDSDCGAFVLQYCKHLAL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative 37; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    CFE712B6AFDAA9D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: December 16, 2002, 19:58:11
Job time : 210 secs
                                                                                                                                                                                                                                                                                                                                                                                                                    75912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.1%;
EMBL; Z99263; CAB16425.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      694 AA;
              EMBL; AL583923; CAC
HSSP; O87703; 1B04.
                                            Leproma; ML1705;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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13;

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SUMMARIES
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AAC48444
AAC40619
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ABV27975
                                                                                                                                                                                                                                                                                                                                                             AAF54830
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                                                                       (first entry)
                                                                                                                                                                                                                                                                                                   10734
13525
695
631
33954
                                           Length
                                                                                                                             10-MAR-2000
                                                                                   1751
1751
1702
1702
1699
1699
16494
1642
755
782
755
611
611
611
474
456
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289
261.5
259.5
255.5
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310.5
308
307.5
307.5
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No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgn2_1/USPTQ_spool/US09848852/runat_16122002_132039_19101/app_query.fasta_1.519
-Q-/cgn2_1/USPTQ_spool/US09848852/runat_16122002_132039_19101/app_query.fasta_1.519
-Q-/cgn2_1/USPTQ_spool/US09848852/runat_1612001
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=bloaum62 -TRANS-bnumn40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=0S09848852_cGN_1_1_281_crunat_16122002_132039_19101 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEGUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
                                                                                               (without alignments)
2500.547 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N. Geneseq_101002:*

| SIDS2/gcgdata/geneseqn-embl/NA1980.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1981.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1982.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1982.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1983.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1985.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1986.DAT:*
| SIDS2/gcgdata/geneseqrgeneseqn-embl/NA1986.DAT:*
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Copyright (c) 1993 - 2002 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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Human protein phos Human; secreted protein; treatment; nutritional activity; cytokine; cell proliferation; cell differentiation; hematopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition; ALIGNMENTS therapy; gene

Homo sapiens

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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AZ43777-Z43808 represent the polynucleotides described in the invention which encode the proteins represented in AAY50905-Y50947.
                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding secreted human proteins, derived from human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                         uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa
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/product= "SENP3"
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                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosoppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                      assays for receptor activity, with the sequence data for this patent did not form part of the printed Note: The sequence data for this patent did not form part of the printed
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Zhang J;
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Yang Y,
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                                                                                                                                                       Ma Y,
Xue AJ,
                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                    Asundi V, Chen R, Ma Y, Wehrman T, Xu C, Xue AJ Goodrich R, Drmanac RT;
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Matches:
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2000US-0552317.
2000US-0598042.
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2000US-0652191.
2000US-0662191.
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                                                                                                       2000US-0727344
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                                                                                                                                                    Liu C, A
Wang Z, W
                                                                                                                               (HYSE-) HYSEQ INC.
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Query Match:
                                                                                                                                                                                                               P-PSDB; AAM39269
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                                                                              14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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19-JUL-2000;
03-AUG-2000;
26-DEC-2000;
                       21-JAN-2000;
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Wang J, W
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                                                                                                                                                                                                                        The present sequence encodes a human de-sentrinase (SENP) 3 polypeptide. The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleolus, SENP3 is found in the nucleolus, and SENP3 is found in both locations. SENP3 is found in both locations. SENP3 polypeptides are sentron-specific proteases that remove sentrin from some sentrinites perificially proteins modified by ubiquitin or NEDB8. SENP polypeptides are used to identify specific modulators of SENP. These modulators are potential anti-proliferative and anti-viral agents such as herpes simplex-1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in the blological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polynucleotides are used as hybridisation probes and amplification primers for detecting gene expression or preparing mutated sequences.
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                                                                                                                                                               New polynucleotide encoding de-sentrinase polypeptides, useful antiproliferative or antiviral agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                 605 G; 498 T; 0 other;
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Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID NO:60
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aTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsnTrpLe 160
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ses not include start codon"
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binding partner identification; ss.
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Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID NO:21.
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110
                                                                                                                                                            ThrProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGly 130
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                                                                                                                                                                                                                                                                       LeuGlyThrLeuTyrGlyGlnAsnTrpLeuAsnAspGlnValMetAsnMetTyrGlyAsp 170
                                                                                                                                                                                                                                                                                                                            LeuValMetAspThrValProGluLysValHisPhePheAsnSerPhePheTyrAspLys 190
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foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;

sapiens Ношо

/\*tag= a /product= "Human secreted protein precursor" /product- "Mature human secreted protein" Location/Qualifiers 441..713 441..521 /\*tag= b 522..710 /\*tag= sig\_peptide mat\_peptide

WO200134767-A2

01-NOV-2000; 2000WO-US30036

99US-0163576 27-JUL-2000; 2000US-0221366 05-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC.

SM; Ruben Olsen HS, Shi Y, Soppet DR, Komatsoulis G, 

2001-316492/33. P-PSDB; AAE01682 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

Claim 1; Page 417-418; 540pp; English.

AAA AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode.

CC AAE01744-AAE01163 represent human secreted protein fragments or variants.

CC The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC The secreted proteins can be diagnosed by determining the amount of the new penes. Specific uses are described for each of the 22 genes, then protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders, cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, kidney disorders, gastrointestinal disorders, proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs considers, and inclements, and inclements, and in chambral to partners, and in chambral to partners, and inclements, and in chambral to partners, and in chambral to partners, and inclements, and an a food additive or recentation processing processing properties prometally present stands processing a proders, and inclements, and inclements, and inclements and an exed as a food additive or recentate processing properties prometally processing properties prometally processing properties and properties prometally present stands processing and processing properties and inclements and an exed as a food additive or modelly processing processing processing processing processing processing processing processing processing processing processing processing processing proc present sequence represents a human secreted protein-encoding cDNA of preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA) invention.

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1156 GGAGGTGCACTGGTCCCTCATCTCTGTGAGGCGGCGCGCACCATCACGTATTTCGA 1215
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551 G; 418 T; 0 other;
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324
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Sequence 1934 BP; 423 A; 542 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system suppression. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activition of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, as assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
1396 CCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGCCGGCA 1455
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Zhang J;
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Yang Y,
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                                             Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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Xu C, Xue AJ,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 4200
                                                                                                                                                                                 AAI60211 standard; cDNA; 1804
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2000US-055317.
2000US-0598042.
2000US-0653450.
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2000US-0653450.
2000US-0693036.
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P-PSDB; AAM41055.
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09-JUL-2000;
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19-OCT-2000; 2
29-NOV-2000; 2
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Wang J, W
Zhao QA,
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other;

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                                                                                                                                                                                                                                                                                                         GlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SValHisPhePheAsnSerPhePheTyr-AspLysLeuArgThrLysGlyTyrAspGlyV
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      1804
331
0
                          Conservative:
Mismatches:
                Matches:
       Length:
                                               Indels:
                                                        Gaps:
                                                                          US-09-848-852A-3 (1-332) x AAI60212 (1-1804)
1.4e-187
1699.00
98.22%
98.22%
95.88%
                          Similarity:
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The Inventor Leadure D. 247.9 inver insuman evaluation and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the three the invention and intionally relates to encompasses polypeptides 90% identical and polynucleotides 95% identical comprision and interest of encompasses polypeptides of enventance of the invention and intional part of the invention and intional antigen comprision buman ovarian antigen and host cells comprising human ovarian antigen polynucleotides and polypeptides in diagnosing, comparing prophosing or preventing various ovary and/or beast related disorders. Such conditions include ovarian cancer and breast rancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, colycystic ovary syndrome, ovarian orysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and vaginitis), immune disorders (e.g., congenital and acquired insorders, espiratory disorders (e.g., anaemia), cardiovascular disorders, coppinges may system disorders. Ovarian antigen polypeptides and corrected polynucleotides may also be used in screening for compounds which conditions may also be used in screening for compounds which conditate ovarian antigen expression or activity. The polynucleotides may also the used for gene therapy, chromosome mapping, in the identification of individuals and in forenic analysis, and the
                                                                                                                                                                                                                                                                                                                      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gestrointestinal disorder; urinary system disorder; drug screening; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to 2175 novel human ovarian antigens (ABP41054-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acid molecules encoding novel ovarian polypeptides,
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                        525 GGCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTG 485
                                                                                                                                                                                                                                                                                Human ovarian antigen HOFOB27 cDNA, SEQ ID NO:96
  rgGlnIleTyrLysGluLeuCysHisCysLysLeuThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 96; 2922pp; English.
                                                                                                                                        BP.
                                                                                                                                     ABQ54216 standard; cDNA; 1933
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P-PSDB; ABP41139.
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                                                                                                                                                                                   ABQ54216;
319
                                                                                                               ABQ54216
                                                                                         RESULT
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
            userur in disease diagnosis, drug targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the invarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    975 CAACGACCAGGTGATGAACATGTACGGAGACCTGGTCATGGACACGGTCCCGGAGAAGGT 1034
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polypeptides may be used as food additives or to prepare antibodies
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                                                                                                                                                                                                                                                                                                                                                     556 ACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCA
                                                                                                                                                                                                                                                                                                                                                                                            sLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGlyLeuValLeuGl
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                                                                                                                                                                                                                                                                     1 MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAla-HisLeuAl
                                                                                                                                                                                                                                                                                                CTGTACTCTTCCCAATGGCTTTGGGGGACCCCCGGGCCAGAAGGGGGAGCGGGTCTGGC
                                                                                                                                                                                                                                                                                                                                                                              nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                   sAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAs
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                                                                                                                                                                                                                                                                                                                            aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl
                                                                                                                                                                                                                                                                                                                                       Sequence 1933 BP; 423 A; 541 C; 551 G; 418 T; 0 other;
                                                                                                                                                1933
323
2
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Mismatches:
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Matches:
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                                                                                                                                                1.27e-184
1674.00
97.60%
97.00%
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Best Local Similarity:
                                         invention.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system as and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scienosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
ä
                                                                      TGTGGCCAGGCAGAATAATGACAGTGACTGCGGTGCCTTTGTGTTTACAGTACTGCAAGCA 1394
                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                    peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease, Hauntington's disease, haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful for treating disorders
                                                                                                sLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMetProLysLeuArgArgGl
                                                       Ren F, W
Zhang J;
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Yang Y,
                                                                                                                                                                    nIleTyrLysGluLeuCysHisCysLysLeuThrval 332
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Xu C, Xue AJ,
, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 629; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liu C, Asundi V, Chen R,
Wang Z, Wehrman T, Xu C,
Zhou P, Goodrich R, Drman
                                                                                                                                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 629
                                                                                                                                                                                                                                      AAI58426 standard; cDNA; 2029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000, 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-058042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-065450.
14-SEP-2000; 2000US-0652191.
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                                                                                                                                                                                                                                                                                               (first entry)
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P-PSDB; AAM39270.
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and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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                                                                                                                                                                                                                                                                                                    sAlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAs
                                    The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                              other;
                                                                                             2029
314
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18
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Mismatches:
Indels:
                                                                 T; 0
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Matches:
                                                                 G; 456
                                                                                                                                             Gaps:
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                                                                  460 A; 560 C;
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                                                                                             6.39e-181
1642.50
94.29%
94.29%
92.69%
                                                                  BP;
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Best Local Similarity:
                                                                  Sequence 2029
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprises a 3'-end sequence to polynucleotide comprises a 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises as 1-end sequence, where the oligonucleotide comprises and the comprise of the 5'-end sequence/3'-end sequence is selected from those defined in the seculional and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13633 to DNAs assily without any specialized methods.
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                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer; detection; diagnosis; antisense therapy; gene therapy;
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1414 GGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAAATG--
                                       nValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeuGlnTyrCysLysHi
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Otsuki
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                                                                                                                                                                                                             Hayashi K, Sa
A, Nagai K,
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T, Wakamatsu A,
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                                                                                                                                                                                                                                                                                                        AAH13708 standard; cDNA; 1578
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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Sugiyama T,
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09-JUN-2000;
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
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                                           439 G; 428 T; 0 other;
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186
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                                           Sequence 1578 BP; 339 A; 372
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50.00%
47.45%
46.28%
                      of the present invention.
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	Oy 100 LysLeuG                 Db 548 AAGCTGGA
	Qy 120 GlnLeuI
	Db 488 CAGCTNAT
	Oy 140 AlaTyrLy
	Db 428 GCTTATA
	Oy 160 LeuAsnAs
	Db 368 CTCAATG
	Oy 180 Val
	Db 308 GIAGGCC
	191
	257
	211
	DD 19/ AGAGAGG RESULT 12 AAH99558 ID AAH99558 star
	AC AAH99558
The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tunnour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.	
	KW antiaggregand KW dermatologics KW neuroprotecti KW immunostimula KW antianaphylac

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaquegant; haemostatic; uulnerary; antiulcer; osteopathic; eczemn; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
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                                                                                                                                                           SerAlaGlnArgPheTrpGlyThrIle-TrpAlaArgArgGlyAlaHisLeuAl
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 17
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Indels:
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287

407 216 467 527 256 587 276 644

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Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
                         ----AATAGAAAACCA 176
                                                                                                                                                                                                                                                                                                       ProlleHisLeuGluValHisTrpSerLeuIleSerValAspValArgArgArgThr11e 236
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                                                                                                                         177 TTTATCAATAGGGAAATAACAAACTATCGGGCCAGACATCAAAAATGT-----AAC
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                                                                        LeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGly
                                                                                                                                                                                                    TCATTTTATGATTCCCAAGGCATTCATTTTAAGTTTTGTGTAGAAGTATATAAGAAAGTAT
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     AAS25529/c
ID AAS25529 standard; cDNA; 503
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28-MAR-2000; 2000US-0192745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibatcherial; endocrine; cardiant; central nervous system; virucide; antibatcherial; endocrine; cardiant; central nervous system; virucide; antibatcherial; endocrine; cardiant; central nervous system; virucide; antibatcheria; unimatagen; cardiovascular; antidaperic; antidaperic; cytostatic; neuroprotective; antidepressant; noctropic; antidabetic; cytostatic; neuroprotective; antidepressant; noctropic; antidaperic; cytostatic; neuroprotective; antidepressant; noctropic; antidaperic; cytostatic; neuroprotective; antidepressant; noctropic; antidaperic; cytostatic; neuroprotective; antidepressant; noctropic; cardidaperic; cytostatic; neuroprotective; antidepressant; noctropic; cardidaperic; cytostatic; neuroprotective; antidepressant; noctropic; cardidaperic; cytostatic; and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis; of disorders associated with the activity of a protein e.g. inflammation, rheuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, cereaning immaning, plateled disorders, thrombocytopeenia, wounds, placers, or anamina, plateled disorders, immondaficion, cereaning immaning, under anamina, plateled disorders, immondaficion, cereaning consisting immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immaning, immanin
genetic disease; haematopoietic disorder; platelet disorder; asthma; thromborytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 ValValGluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGly 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  depression,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis, severe combined immunodéficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depressi
Alzheimer's disease, Parkinson's disease, neurodegenerative and
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Mismatches:
Indels:
Gaps:
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Matches:
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2000US-0488725.
2000US-0552317.
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755.50
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                                                                                                                                                   Homo sapiens.
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AAI84371;

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of ovarian cancer. The compositions used none or more ovarian tumnous proteins, their associated polynucleotides, or immunogenic portions of the proteins. The ovarian tumnour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumnour protein. They are also useful for inhibiting the development of cancer in protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumnour DNA or protein by incubating isolated T-cells allowing them to proliferate, for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutant species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS2539
                                                                                                                                                                                   The invention comprises compositions used for the therapy and diagnosis
                                                               New polynucleotides encoding ovarian tumour proteins, useful for
treating ovarian cancer, and as probes, primers, and markers of cancer
progression -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 CAGGGCTGGAAAGGTTACTTCAAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 503 BP; 120 A; 110 C; 147 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     represent human ovarian tumour protein cDNA clones.
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                  Example 1; page 375; 378pp; English.
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661.50
88.03
88.03
37.33
                                              WPI; 2001-488879/53
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                 Algate PA,
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis requiating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesls; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 GlyTyrAspGlyValLySArgTrpThrLysAsnValAspIlePheAsnLySGluLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4431; 1399pp + Sequence Listing; English.
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18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
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                                                     257 -----TACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATG 310
122 ACCATCACCTATTTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCC 181
                                                                                                                                                             GlyTyrPheLysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheVal 294
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Human; neuroblastoma; malignancy
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The invention relates to novel or human neuroblastoma. The nucleis of human neuroblastoma. The nucleis of human neuroblastoma. The nucleis of consense in diamosing the prognous susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators or tuned susceptibility indicators 
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Indels:

1.18e-61 614.00 72.07% 67.12% 34.65%

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Pred. Score: Query Match:

US-09-848-852A-3 (1-332) x AAI93958 (1-820)

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24
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Pred. No. is the number of results predicted by chance to have a

ALB34294 HOMO Sapi AF199459 HOMO Sapi AY008763 HOMO Sapi AX081143 Sequence AL050283 HOMO Sapi AY008764 MUS muscu AF194031 MUS muscu AC016876 HOMO Sapi AX209870 Sequence AX209812 Rattus no AL603707 Mouse DNA AK000923 Homo sapi AB060892 Macaca fa AC119115 Rattus no AL80532 Mus muscu AC099294 Rattus no AB07445 Macaca fa AC099436 Rattus no BC008589 Homo sapi AC09765 Rattus no AC125091 Mus muscu AC119115 Rattus no AC125091 Mus musculu AC103148 Rattus no AC2873 Mus musculu AC103148 Rattus no AC2873 Mus musculu AC103148 Rattus no AC103148 Rattus no AC103148 Rattus no BC023129 Mus muscu AXB1135 Sequence AX143770 Homo sapi AJ34385 Homo sapi AJ34384 Homo sapi AR368904 Mus muscu BC031652 Mus muscu Homo sapi Pan trogl Canis fam Canis fam Felis cat Sus scrof Bos tauru AF260129 Rattus no Papio cyn Sequence Pan trogl Pan trogl score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description AC129071 FAC127470 FAC127470 FAC127470 FAC12746 FAC129071 FAC12623 FAC12623 FAC12623 FAC12623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 FAC13623 SUMMARIES AL806532 AC099294 AC099294 AC07445 BC008589 BC008589 AC030705 AC125091 AC125091 AC121115 AC13118 ACMOS32 HSM805332 AF199459 AY008763 AX081143 HSM800198 AF194031 AC016876 AC016876 AC129071 AC127470 AC127470 AC12632 AC12632 AC12632 AC126337 AC126337 AC126337 AC126337 AC126337 AC126337 AC126337 AC126337 AC126337 AC126337 BC023129 AX081135 AF149770 HSA343855 HSA343584 AF368904 BC031652 AL603707 AK000923 AF260129 AB060892 AC119115 10 DB 164504 215795 173588 161428 203281 139405 2793 76754 333300 138792 182718 209237 2903 6732 164504 503 184026 2673 251835 Match Length 1707 177555 153553 2007 138792 257644 209237 Query Score 522.4 486.4 477.4 474.4 474.4 469.6 442 427.6 426 344.6 333.4 301.6 277.4 260.4 254.6 253.8 251.4 251.4 230.6 183.4 182.4 176 143.8 101.4 98.4 96 83.8 83.8 83.2 83.2 81.6 1843.4 1692.4 1459. Result õ υo 000

ALIGNMENTS

Homo sapiens
Exkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2269)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

REFERENCE AUTHORS TITLE JOURNAL

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This clone (DKFZp762A152) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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LGTLYGQNMLNDQVMMYGDLVMDTVPEKVHFNSFFYDKLRTKGYDGVKRWTKNVDI
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                                                                                                                                                                                                                                                                                           /tissue_type="melanoma (MeWo cell line)"
/clone_lib="762 (synonym: hmel2). Vector pSportl; host
DH10bs: sites Not1 + SalI"
/dev_stage="adult"
 from S. Wiemann, Molecular Genome Analysis, German Cancer
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               Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de; sequenced by BMF2 (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="DKF2p762A152"
/note="partial similarity to sentrin/SUMO-specific
protease (Homo sapiens)"
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Bukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2258)
Choi, S.J., Jeon, Y.J., Kim, K.I., Nishimori, S., Suzuki, T., Uchida, S., Dinect Submission
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                     ATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGTCGGC
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PPMEDGCLRWTPRSTDPDSGLLSCTLDNGFGGQSGPEGERSLAPPASILISNVCSI
GDHVAQELFQGSDLGAAEEARRPGERAGQHSPLREBHYTCVQSILDEFLQTYCSLIPL
STDEVVEKLEDIFQQEFSTPSRKGTVLQLLQSYQRMCGNAWYRGFRVAYRHYLTMD
LGTLYGQNWLNDQVMNYGDLWDLYDEKVHFFNSFYDKLRTKGYDGXRWTKNVDI
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98.98;
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                            AGCTGATCCAGTCTTACCAGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCCGAGTGG
                                                        CITATAAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGC
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/gene-start=1
/product="sentrin/SUMO-specific protease"
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Gong, L. and Yeb, E.T.
Direct Submission
Submitted (04-OCT-2000) Institute of Molecular Medicine, University
of Texas-Houston, 2121 W. Holcombe Blvd. 928, Houston, TX 77030,
OSA
                                                                                                                                                                                                                                                                                                                                                                                    mRNA linear PRI 21-NOV-2000 protease (SENP3) mRNA, complete.
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Catarrhini; Hominidae; Homo.
                                           2214
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1 GCCTCCCTGTCCCCCGACCCTCTTTGATGCCTCAGCAAGTGAAGAGGAGGAAGAAGAGGG
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Pred. No. 0;
0; Mismatches
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Homo sapiens sentrin/SUMO-specific
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Yeh,E.T., Gong,L. and Kamitani,T.
Ubiquitin-like proteins: new wines
Gene 248 (1-2), 1-14 (2000)
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Corganism="Homo sapiens"
/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/gene="SENP3"
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Oy Dp	181	GCTCACAGGGCCGGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA 240 
Qy Dp	241	CCTCGCTGACATTCCACTGGAAGCTTTGGGGGGCGCCACCGGGGGGGG
Qy Db	301 536	CACACCCCAAGAACCATTTCACCCCAGCAAGGGGTGCGACGCCACAGGTGCCATCCC 360
Qy	361	CCTGTTGTCGTTTTGACTCCCCCGGGGGCCACCTCCACCCGGCTGGTTCTGGTAGGTG 420
75 Oy	2 10	TCTCATGCTGAGGATGGGGTGAGAGGTCTCCACAGTGCCCTCTGGGCCCCCCATGGGGTCTCTGGCCCCCCATGGGGGTCTCTCAGGCCCCCCCATGGGGGGGG
Oy Db	481	AGGAAGATGGACTCAGGTGGACTCCAAAGTCTCCTCTGGACCCTGACTCGGGCCTCCTT 540
Qy Db	541 776	CATGTACTCTGCCCAACGGTTTTGGGGAACAATCTGGGCCAGAAGGGGAGCGCA-CTTGG 599 
Qy Db	600	CACCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATGGGGGACCATGTGGCCC 659
Qy	968	AGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCAGAGAGGCCTGGGGAGA 719 
Qy Dp	720	AAGCCGGCCAGCACACCCCTGCGAGAGGAGGACATGTGACCTGCGTACAGAGCATCTTGG 779 
Qy Db	780	ACGAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGA 839
Oy Dp	840 1076	AGCTGGAGGACATTTTCCAGCAGGAGTTTTCCACCCCTTCCAGGAAGGGCCTGGTGTTGC 899 
Qy	900	AGCTGATCCAGTCTTACCAGCGGATGCCAGGCAATGCTGAGGGGCTTCCGAGTGG 959
Qy	960 1196	CTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGC 1019 
Oy Dp	1020 1256	TCAATGACCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACACTCCCTGAAAAGG 1079 
Qy Db	1080 1316	TGCATTTCTTCAATAGTTTCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGTGA 1139 
Qy Db	1140	AAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCATCCACC 1199 
οy	1200	TGGAGGTGCATTGGTCCCTCATCTCTGTGAGGCGACGCACCATCACCTATTTG 1259

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PAT 27-FEB-2001
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Enkaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 2206)
Gong, L. and Yeh, E.T.
Composition and methods relating to senpl - a sentrin-specific protease
Partent: WO 0109292-A 9 08-FEB-2001;
Board of Regents, The University of Texas System (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                       1616 ATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGC
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Sequence 9 from Patent W00109292.
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                                                                                           GGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGCCCCACTCATCGAAAAACCT
                                                                                                                   GCTCACAGCGCCGCCGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
                                                                                                                                          AGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCCAGAGGCCTGGGGAGA
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ed. No. 0;
Mismatches
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612 c 605 g 499
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Pred.
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This clone (DKF2p586K0919) is available at the R2PD in Berlin. Plass contact the R2DD: Ressourcenterery Weburder (14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mlps.blochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1782)
Wiemann,S., Well.B., Wellenreuther,R., Gassenhuber,J., Glassl,S., Ansorge,W., Boecher,M., Bloecker,H., Bauersachs,S., Blum,H., Lauber,J., Duesterhoeft,A., Beyer,A., Koehrer,K., Strack,N., Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,D., Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs
                                                                               1782 bp mRNA linear Fra 1. DKFZp586K0919 (from clone DKFZp586K0919);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Wiemann, S.
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/clone_lib="586 (synonym: hutel). Vector pSportl; host
DH10B; sites NotI + Sall/Mlul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
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Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J.
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/gene-"DKPZp586K0919"
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/db_xref="taxon:9606"
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                                                                                                                              Homo sapiens mRNA; cDNA complete cds.
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Direct Submission
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Matches 1734; Conservative
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                                                               72 GGCCTCGCACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGTGCGACGCCACAGGTG
                                                                                       354 CCATCCCCCTGTTGTCGTTTTGACTCCCCCCGGGGGCCACCTCCACCCCGGCTGGGTCTG
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WKGYFRMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
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Yeh, E.T., Gong, L. and Kamitani, T. Objquitin-like proteins: new wines in new bottles Gene 248 (1-2), 1-14 (2000)
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Gong, L. and Yeh, E.T.
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LIPHLEVHWSLISYDVRRTTTTPDSQRTLANRFCRHIAKTGARANKENELDFHQG
WMGYFRMNVARQNNDSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1707)

Nishida.T., Tanaka, and Yasuda, H.

A novel mammalian Smt3-specific isopeptidase 1 (SMT3IP1) localized in the nucleolus at interphase

Bur. J. Biochem. 267 (21), 6423-6427 (2000)

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Horinouchi, Hachioji, Tokyo
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Pred. No. 1.4e-303;
0; Mismatches 135;
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13   GAGGCAACTGCGAGCCGCCCCCCCCCCAACAAAAACT   136   16   16   16   16   16   16   16   1		1	1
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347 GTCCAGGGCCCGCGCCGCGCCCGGGGCCGGGGCCGGGGCCGGGGCCGGGG		181	24
241 CCTCGCTGACATTCCACTGAAGCTTTGGGGGCGCCACGGGGCGGGGGCCTCG 300 407 CCTCGCTGACATTCCACTGAAGCTTTGGGGGCGCCACGGGCGGG		347	40
4.07 CCTCGCTGACATTCCACTGGAAGCTTTGGGGGCGCCCCGAGGCGGGGCGCGCACCGCGAACTTCG 301 CACACCCCAAGAACCTTCACCCCCAGGAAGGGGTGCCACCGGCGCGCGC		241	CTCGCTGACATTCCACTGGAAGCTTTGGGGCGCCCACCGGGGCCGGCGGGGGCCTCG 30
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467 GGCACCCCAAGAACCATCTCTCACCCCAGGAGGGGTGCAACGCCACAGGTGCCATCAC 361 CCTGTTGTTTTTGACTCCCCCGGGGGCCACCCCGCTGCGTGGTGTGTTGTAGTG 262 CCTGTTGTTTTTGACTCCCCCCGGGGGCCACCCCCGCTGGGTGTTGTTAGTGTGTAGTG 263 CCTGTTGTTTTTGACTCCCCCGGGGGCCACCCCCGGTGGGTG		301	36
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1111		361	CTGTTGTCGTTTTGACTCCCCCGGGGGCCACCTCCACCCCGGCTGGGTCTGCTAGTG 42
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481   AGGAAGATGGACTCAGGACTCCTGGACCTGACTCGGCCTCTTT   540		587	64
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720 AAGCCGGCCAGCACACCCCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGG 779 111   111		827	88
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947 ATGANTTCTTCAAACTTATGGCGCCTCATCCCTCTCACCACTGATGAATTGTAGAA 100 840 AGCTGAATTCTTCAACACTTATGGCGGCCTCATCCCTCTCACCACTGATGAATTGTAGAA 100 840 AGCTGAAGGACTTTTCCAGGGGATTTTCCACCCCTTCCAGGAAGGGCTTGGTTGC 899 11		780	83
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067 AĞCTGATCCAGTCTTATCAGCGGATGCCAĞGCAACĞCTATĞGTAAĞGGGCTTCCGGGTAT 112 960 CTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGACCTTGTATGGACAGAACTGGC 101		900	95
960 CTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGC 101  1		1067	112
020 FCAATGACCAGGTGAFGAACATGTATGAGACCTGGTCATGGACACAGTCCCTGAAAGG 107		960	101
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080 TGCATTTCTTCAATAGTTTCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGGTGA 113		1187	124
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Mammalia, Eutheria; Firmates; Catarinii; Hominidae; Homio.

RS Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome, clone RP11-186B7

Unpublished

2 (bases 1 to 177703)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Cander, E., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gart, G., Hagos, B., Heaford, A., Horton, L., Howlan, P., PitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Cardyna, S., Gart, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McGurk, A., McGurk, A., McGurk, A., McGuran, R., Macdonald, P., Marquis, N., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Stojanovic, N., Subramanian, A., Talamas, J., Peterson, K., Pollara, V., Riley, R., Sub, A., Santos, R., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Libe, J., Chang, J., Chader, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhalater, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, JS., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Johnson, R., Lindblad-Toh, K., Haratas, A., Kalls, C., Lander, T., Levine, R., Lindblad-Toh, K., Karatas, A., Kalls, T., Lievine, R., Lindblad-Toh, K., Karatas, A., Kalls, T., Lievine, R., Lindblad-Toh, K., Karatas, A., Kalls, T., Lievine, R., Lindblad-Toh, K., Karatas, T., Lievine, R., Lindblad-Toh, K., Karatas, T., Lievine, T., Levine, R., Lindblad-Toh, K., Karatas, T., Lievine, T., Levine, R., Lindblad-Toh, K., Karatas, T., Lievine, T., Levine, R., Lievine, T., Lievine, T., Levine, T., Lievine, T., Lievine, T., Lievine, T., Lievine, T., Le
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Homo sapiens clone RP11-186B7, *** SEQUENCING IN PROGRESS ***, 10
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1140 AAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCATCCACC 1199
                                   1487 AGGCAGTCAAAAAAGACCGACTGGACTTCCATCAGGGCTGGAAAGGTTACTTCAAAATGA 1546
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                                                                                                                    1260 ACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTATCTACAGGCAG
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RESULT 9
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Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Nell,D., Ollver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:15421989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Contact: sequence_submissions@genome.wi.mit.edu
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45967 c 46568 g 41254 t 1052
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Best Local Similarity 96.9%; Pred. No. 2.9e-120;
Matches 562; Conservative 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Catarrhini; Hominidae; Pan.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

I (bases 1 to 164504)

S Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Haghighi, P., Hansen, N., Ho, S.-L., Maduro, V.B.,
Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,
McCloskey, J.C., NcDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Miggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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Pan troglodytes clone RP43-149M23, WORKING DRAFT SEQUENCE, 7
                                  22722 GGGGGTGGCTACAGAAAAGCCCCTTTCCTCTGTTTTGCAGGGGAGTGTGGCCCTGTGG 22663
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1547 TACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAAC 1606
                                                                                                                               TCCAGTTCCTTTCCTCTCTTGCCTCTTCCCACTCACTTCCCTTTGGTTTTTCATATTAA 1666
                                                                                                                                                                                                                                                              ATGITICAATITCTGTATTTTTTTTTTTTGAGAGAATACTTGTTGATTTCTGATGTGCA 1726
                                                                                                                                                                                                                                                                                                                                                                                             GGGGGGGGCCTACAGAAAAGCCCCTTTCTTCTTCTTGCAGGGGAGTGTGGCCCTGTGG 1786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: NIH Intramural Sequencing Center
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Contact: nisc_zoo@nhgri.nih.gov
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HTG: HTGS_PHASE1; HTGS_DRAFT.
Pan troglodytes
Pan troglodytes
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181 GCTCACAGGGGCGGCGGCGAGGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
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                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 159951 bases at least Q40 consensus quality: 161126 bases at least Q30 consensus quality: 161900 bases at least Q20 lnsert size: 185000; agarose-fp lnsert size: 163904; sum-of-contigs Quality coverage: 7.39x in Q20 bases; sum-of-contigs Quality coverage: 8.34x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence: It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
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?.2e-119;
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tive 0; Mismatches
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42831 c 41755 g 40472
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Matches 531; Conservative
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Chimpanze...

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1 (Dases 1 to 215795)

SAkhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,

Lee-Lih, S.-Q., Legaspl, R., Maduro, O.L., Maduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,

McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,

Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,

Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                              24696 CTCTCATGGCTGAGGATGGGGTGAGAGGTCTCCACCAGTGCCCTCTGGGCCCCCCATGG 24637
                                                                                                                                                                                                                                           301 CACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGTGCGACGCCACAGGTGCCATCCC 360
                                                                                                                                                                                                                                                                                                                                                                                         CCTGTTGTCGTTTTGACTCCCCCCCGGGGCCCACCTCCACCCCGGCTGGGTCTGCTAGGTG 420
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Submitted (17-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
24936 GCTCACAGCGCCGCCGCCGCGCGCGTGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
                                                                                                                                          24816 CACACCCCAAGAACCATCTTTCACCCCAGGAAGGGGGTGCGACGCCACAGGTGCCATCCC
                                                                                                    241 CCTCGCTGACATTCCACTGGAAGCTTTGGGGGCGCCACCGGGGCCGGCGGCGGGGGCCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center close name: 145013

Center close name: 145013

Center close name: 145013

Center close namery Statistics

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 203929 bases at least Q40

Consensus quality: 208855 bases at least Q20

Insert size: 190000, agarose-fp

Insert size: 14395; sum-of-contigs

Quality coverage: 7.30x in Q20 bases; agarose-fp
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Contact: nisc_zoo@nhgri.nih.gov
------ project Information
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AUTHORS
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                      NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Quality coverage: 6.47x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                              f unknown length
g of 9036 bp in length
if unknown length
of 05275 bp in length
if unknown length
g of 8962 bp in length
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gap of unknown length
contig of 15560 bp in length
gap of unknown length
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gap of unknown length
contig of 14902 bp in length
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of 15915 bp in length
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of 10030 bp in length
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unknown length
of 4308 bp in length
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Cercopithecinae; Papio.
S. Akter, N., Antonellis, Ayele, K., Beckstrom-Sternberg, S.M.,
S. Akter, N., Antonellis, Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Madrian, S.D.,
McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,
Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC127468 173588 bp DNA linear HTG 17-JUL-2002 Papio cynocephalus anubis clone RP41-263F8, WORKING DRAFT SEQUENCE, 13 unordered pieces. AC127468.1 GI:21886864 HTG: HTGS_DRASE1; HTGS_DRAFT.
                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                 Db 205638 GCCTCCCTGTCCCCGACCTCTTTTGATGCCTCAGCAAGTGAAGAGGAGGAAGAAGAGG 205697
                                                                                                                                                                                                                                                                                                                                                                                                         Db 205698 AGGAGGAGGAGGATGAAGATGAAGAGGAGGAAGGAGCTAGCAGCTTGGAGGCTGCCCCCAAGAT 205757
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                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 205758 GGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCTTCCCGCCCACTCATCGAAAACCT
                                                                                                                                                                                                                                                           Db 205818 GCTCACAGCGCCGCCGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
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Papio cynocephalus anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                        Length 215795;
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                                                         1511 others
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                                                                                                                                        Score 530.4; DB 2;
Pred. No. 2.3e-119;
0; Mismatches 1;
                           /note="assembly_fragment"
52160 a 54859 c 53752 g 53513 t
166903. .215795
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                                                                                                                                           26.6%;
99.8%;
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Matches 531; Conservative
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ACCESSION
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AX069229
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KEYWORDS
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                                  Sequencing Center, 8717
                                                                                                                                                                                        Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 167086 bases at least 040
Consensus quality: 167086 bases at least 020
Consensus quality: 16822 bases at least 020
Insert size: 177000; agarose-fp
Insert size: 17388; sum of-contigs
Quality coverage: 6.54x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68520: gap of unknown length
84235: contig of 15715 bp in length
84335: gap of unknown length
112003: contig of 27668 bp in length
112103: gap of unknown length
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1.173588
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unknown length
of 9729 bp in length
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of 17601 bp in length
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of 4393 bp in length
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contig of 3572 bp in length
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/clone="RP41-263F8"
/clone_lib="RP41"
1. .2699
/note="assembly_fragment"
                                                                               Center: NIH Intramural Sequencing Center
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              Direct Submission
Submitted (17-JUL-2002) NIH Intramural Seq
Grovemont Circle, Gaithersburg, MD 20877,
                                                                                                             Web site: http://www.nisc.nih.gov
                                                                                                                               Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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/note="assembly_fragment"
11656. .15227
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15328. 19720
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Center clone name: 263F08
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                TITLE
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AUTHORS
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Momo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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WO0102594.
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40991. .50719
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AX069229
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                     clone_end:SP6
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Best Local Similarity 98.9
Matches 526; Conservative
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multiple regulatory elements that direct high-level reporter gene expression in mammalian cell lines Genomics 62 (3), 468-476 (1999)
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4773. .5193
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5249. .>6732
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656. 1019
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/rpt_type=dispersed
1521. .1823
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/rpt_type=dispersed
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/gene="EIF4A1"
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ilarity 94.9%;
Conservative
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The human eukaryotic initiation factor 4AI gene (EIF4AI) contains
                                                                                                                                                                                                                                                                   1606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCC 1486
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HOMO sapiens eukaryotic initiation factor 4AI (EIF4AI) gene,
partial cds.
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                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                             Length 5318;
                  and Ford, M.J.
                                                                                                                        others
                                                                                                                                                                                      Indels
 1 (bases 1 to 5318)
Greaves, D.R., Thomsen, L., Catchpole, I.R. and For Dna constructs based on the eif4a gene promoter Patent: WO 0102594-A 40 Il-JAN-2001;
GLAXO GROUP LIMITED (GB).
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                                                                                                                                                            Score 486.4; DB 6;
Pred. No. 9.8e-109;
1; Mismatches 17;
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                                                                                                                       1350
                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
1210 c 1423 g 1350
                                                                   Location/Qualifiers
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AF175325.1 GI:696997
                                                                                                                                                            Query Match 24.4%;
Best Local Similarity 94.9%;
Matches 544; Conservative
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Greaves,D.R. and Catchpole,I.
Direct Submission
Submitted August William Dunn School of Patholog
University of Oxford, South Parks Road, Oxford OX1 3RE, UK
Location/Qualifiers 11; Length 6732; factor 4AI" others Indels /product="eukaryotic initiation factor 4
/protein\_id="AAF34151.1"
/db\_xref="G1:6969998"
/translation="MSASQDSRSRDNGPDGMEPEGVIIE"
6681. 6732
/gene="EIF4A1" 3868. 4120 /note="similar to murine eIF-4AI gene" 4259. 4334

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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1 (bass 1 to 164504)

1 (bass 1 to 164504)

1 (bass 2 to 164504)

1 (bass 1 to 164504)

2 Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,

Benjamin, B., Blakesley, R.W., Boulfard, G.G., Breen, K., Brinkley, C.,

Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,

Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,

McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,

Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,

Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

I. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC129071 164504 bp DNA linear HTG 25-JUL-2002 Pan troglodytes clone RP43-149M23, WORKING DRAFT SEQUENCE, 7 unordered pieces.
1786 G-CCTGGGTGGAGCAGTCATCCTCCCCCTTCCCGTGCAGGGAGCAGGAAATCAGTGCT- 1843
                                                                                                                                                                             4095 AGGGGATGGCTACAGAAAGCCCCTTTCTTCCTCTTTGCAGGGGAGTGTGGCCCTGTG 4154
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Submitted (25-JUL-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Center clone name: 149M23

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 159991 bases at least Q40
Consensus quality: 161900 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 183004; sum-of-contigs
Quality coverage: 7.39x in Q20 bases; sum-of-contigs
Quality coverage: 8.34x in Q20 bases; sum-of-contigs
                                                               AGGGGGTGGCTACAGAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGCCCTGTG
                                                                                      Center: NIH Intramural Sequencing Center
Center code: NISC
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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DEFINITION
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 2.4e-106;
0; Mismatches 6;
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42831 c 41755 g 40472 t

    .164504
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1. 3137
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/note="assembly_fragment"
13973. 19270
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30685. .45302
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contig of 9429 bp in length
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contig of 8629 bp in length
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/db_xref="taxon:9615"
/clone="RP81-332E11"
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/note="assembly_fragment"
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/note="assembly_fragment"
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                           AC126925 161428 bp DNA linear HTG 10-JUL-2002 Canis familiaris clone RP81-332E11, WORKING DRAFT SEQUENCE, 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
Db 136003 GGGGGTGGCTACAGAAAAGCCCCTTTCTTCTTCTTGTTTGCAGGGGAGTGTGGCCCTGTGG 136062
                                                                         Db 136063 ccredegregaccagrearcerececerrecereregeageageagaarcagregreg 136122
                                                                                                                                        Db 136123 GGTGGTGGGCGGACAATAGGATCACTGCCTGCCAGATCTTCAAACTTTT-TTTTTTA 136181
                                       CCTGGGTGGAGCAGTCATCCTCCCCTTCCCCGTGCAGGAGCAGGAAATCAGTGCTGGG 1846
                                                                                                                 Center clone name: .wr
Center clone name: .wr
Center clone name; 322E11
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 18712 bases at least Q40
Consensus quality: 153125 bases at least Q20
Insert size: 152000; agarose-fp
Insert size: 160028; sum-of-contigs
Quality coverage: 5.36x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: cwp
                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                          AC126925.1 GI:21724102
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AC126925/c
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of 10205 bp in length unknown length of 14362 bp in length

unknown length of 9267 bp in length

LOCUS

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unknown length of 8902 bp in length

of 8880 bp in length

bp in length bp in length

of 4836 of 6670 unknown unknown

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of 8718 bp in length

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length length

in length

unknown leng of 3852 bp i unknown leng

Gaps Length 161428; . 0 1406 others Indels Score 474.4; DB 2; Pred. No. 1.3e-105; 0; Mismatches 36; /note="assembly\_fragment" /note="assembly\_fragment" /1863 c 41233 g 37340 t /note="assembly\_fragment" Query Match 23.8 Best Local Similarity 93.2 Matches 496; Conservative

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88136
                120
                                180
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                                                 240
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                                121 GGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGGCCCCACTCATCGAAAAACCT
                                                 GCTCACAGCGCCGCCGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAAAGCA
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Search completed: December 16, 2002, 17:29:13 Job time : 6622 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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December 16, 2002, 21:18:11; Search time 2422 Seconds (without alignments) 2220.025 Million cell updates/sec
                                                                                                                                                                        1 MYSAQRFWGTIWARRGAHLA......DMPKLRRQIYKELCHCKLTV 332
OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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                                         Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

16154066 segs, 8097743376 residues

Searched:

32308132

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-DOCALIGN=200 -THR\_SCORE-pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NRM=xt -HEAPSILE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09848852\_eCGN\_1\_1\_2024\_erunat\_16122002\_132040\_19159 -NCPU=6 -ICPU=3
-NO\_XLDXY -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -LONGLOG -DEV\_TIMEOUT=120
-WARN\_INMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Command line parameters:

em\_estov:\*
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em\_htc:\*
gb\_estl:\* em\_estba:\* em\_esthum:\* em\_estin:\* em\_estmu:\* EST:\* Database :

em\_gss\_other:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_mus:\* em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_gss\_pln:\* em\_estfun:\* em\_gss\_vrt: em\_estom:\* gb\_est2:\* gb\_htc:\* gb\_est3:\* gb\_est4:\* gb\_est5:\* db\_gss:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	(	Query		1		1
2	Score	Match	Length	DB	QI	Description
	13	78.	1071	14	BM806659	59 AGENC
	13	77.	0	14	BM806502	GENC
	12	70.	804	12	BG870520	50275
	1172	. 99	728	12	BG865703	5027€
	11	63.	985	13	BI456217	50317
	10	61.	626	14	BM696661	BM696661 UI-E-DWC
	10	.09	905	14	BQ898865	BQ898865 AGENCOUR
	985	55.	1134	14	BM804530	BM804530 AGENCOUF
υ	6	55.	667	17	AZ399027	AZ399027 1M0164L10
c J	6	55.	616	10	AW916790	AW916790 EST34819
_	1 9	53.	620	10	AW578424	AW578424 RC1-CT02
-	2	53.	620	10	AW604359	AW604359 RC1-CT02
1	3	52.	572	10	BE077141	BE077141 RC5-BT06
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-	6	51.	549	13	BM507574	BM507574 ih41e03.
	7	64	593	10	AW643059	AW643059 cm25f04.
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-	. 6	48.	545	17	A0978128	A0978128 RPCI-23-
	. 0	47.	504	12	BF954315	BF954315 OV2-NNOC
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1 (2)	20	46.2	477	10	LO AW825381	AW825381 us14e04.y
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7	7 7	45.	442	6	AA549588	AA549588 vk76e01.s
(1	7	45.	689	12	BF608506	BF608506 MY1_0014
(3	7	44.	472	14	BM821282	BM821282 K-EST009
œ	0 7	44.	φ	14	BM829799	BM829799 K-EST010
ص د	1 7	44.	1070	13	BI247525	BI247525 60296016
(*)	2 7	44.	œ	11	BC000958	BC000958 Homo sap
(*)	3 7	44.	œ	11	AF335474	AF335474 Homo sap
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BM806659 1071 bp mRNA linear EST 05-MAR-2002 AGENCOURT\_6542888 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5548958 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1071)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC) 5', mRNA sequence. BM806659 BM806659.1 GI:19123482 human. EST KEYWORDS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS TITLE ACCESSION VERSION BM806659 LOCUS

ALIGNMENTS

RESULT 1

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248 ArgCysProLysHisIleAlaLysTyrLeuGlnAlaGluAlaValLysLysAspArgLeu
                                                                                                                                                                                                                                                                                                            DEFINITION
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TITLE
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                                               cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM12258 row: 1 column: 15
Plate: LLAM12258 row: 1 column: 15
High quality sequence stop: 648.
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       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1060)

S 1 (bases 1 to 1060)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

L Onpublished (1999)

L Ontact: Robert Strausberg, Ph.D.

Email: cgapbs-refmail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONTact: Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1228 row; h column: 18

High quality sequence stop: 652.

Location/Qualifiers

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AGENCOURT_6542932 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548865
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MetTyrSerAlaGlnArgPheTrpGlyThrIleTrpAlaArgArgGlyAlaHis-LeuAl
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/note="Organ: salivary gland; Vector: p
                              Contact: Robert Strausberg, Ph.D.
Email: gqapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Gistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAM10842 row: n column: 09
High quality sequence stop: 789.
Location/Qualifiers
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   Health, Mammalian Gene Collection (MGC)
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NIH-MGC http://mgc.nci.nih.gov/.
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                 ATGTACTCTGCCCAACGGTTTTGGGGGACAATCTGGGCCAGAAGGGGAGCGCAGCTTGGC
                                                       aProProAspAlaSerIleLeuIleSerAsnValCysSerIleGlyAspHisValAlaGl
                                                                                                                             nGluLeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLy
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mRNA sequence.
BG870520
BG870520.1 GI:14221060
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97

134 157 154 217 277

337 214 397 234 457 254 517 274 577

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GluGluHisValThrCysValGlnSerIleLeuAspGluPheLeuGlnThrTyrGlySer
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COMMENT
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/Organism="Mus musculus"
/Strain="FVB/N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="InAGE:400938"
/clone="InAGE:400938"
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/note="Organ: Salix Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

168 C 186 g 176 t
                                                                                                                                                                                          BG865703 728 bp mRNA linear EST 29-MAY-2001 02783877F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4909938 5',
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HT-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAMIGO9 row: j column: 19
High quality sequence stop: 728.
                                     637
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                         294 LLeuGlnTyrCysLysHisLeuAlaLeuSerGlnProPheSerPheThrGlnGlnAspMe
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Matches:
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                                                                                                                                                                                                                   mRNA sequence.
BG865703
BG865703.1 GI:14216243
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1172.50
97.53%
96.30%
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Best Local Similari
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TITLE
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 985)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIG37 row: o column: 24
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                                                                                                                                                                                                                                                                                                                                                                                                       169 GlyAspLeuValMetAspThrValProGluLysValHisPhePheAsnSerPhePheTyr 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuIleProLeuSerThrAspGluValValGluLysLeuGluAspIlePheGlnGlnGlu
                                                                                 ProGlyAsnAlaMetValArgGlyPheArgValAlaTyrLysArgHisValLeuThrMet
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Location/Qualifiers
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BI456217
BI456217.1 GI:15246873
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//dev.stage="adult"
//dev.stage="adult"
//dev.stage="adult"
//deb_host="DH10B (Life Technologies) .(Tl phage resistant)"
//note="Organ: eye; Vector: pr773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-DW0 is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pr773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)!B tail. The sequence tag for this library is CGATTAGGGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                       451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 9565
Email: msoares@Ublue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      1 (bases 1 to 626)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UI-E-DWO-agk-m-22-0-UI.rl UI-E-DWO Homo sapiens cDNA clone UI-E-DWO-agk-m-22-0-UI 5', mRNA sequence.
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208
0
0
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0
                                                                                                                                                                                                                                    Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/tissue_type="lens"
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Mismatches:
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Genome Res. 6 (9), 791-806 (1996)
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Best Local Similarity:
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                                                                               human.
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No
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AUTHORS
TITLE
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COMMENT
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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/organism="Mus musculus"
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/lab\_host="DH10B"

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BQ898865
BQ89865.1 GI:22290891
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 11 (bases 1 to 905)
11H-MGC http://mgc.nci.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
171
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13564 row: o column: 14
High quality sequence stop: 614.
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                                                                                                                                        ValMetAspThrValProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeu
                                                                                                                                                                                                                                                                                                                            ProSerArgLysGlyLeuValLeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsn
                                                          192 ArgThrLysGlyTyrAspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLys
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/organism="Homo sapiens"
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/clone="IMAGE:6181093"
/clone=lib="Lupski_dorsal_root_ganglion"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
                                                                                                                                                                                                                                                                                                                                                                         HisileAlaLysTyrLeuGlnAla 259
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/note="Vector: pcMv-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI: cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TGGACCACGCGTCGG-3' and
5'-GACTAGTTCTAGATCGCGAGCGCCCCT(15)-3'. Size selected >
1 Nb for average insert length 1.7 Nb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
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Homo sapiens cDNA clone IMAGE:5554637
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AGENCOURT 6492923 NIH_MGC_85
5', mRNA sequence.
BM804530 GI:19121353
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1073.00
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Best Local Similarity:
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us-09-848-852a-3.rst

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1134)
NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: lymph; Vector: pCNV'SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAML2273 row: i column: 06
High quality sequence stop: 583.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:5554637"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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Conservative:
Mismatches:
Indels:
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                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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"E (bases 1 to 667)

E Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Welss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ399027
1M0164L10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0164L10 R, DNA sequence.
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
180
                                                                                                                  795
                                                                                                                                                              180 lHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyrAsp---GlyVa 199
                                                                                                                                                                                                                                                          160 uAsnAspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysVa
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Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0164 row: L column: 10
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/organism="Mus musculus"
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Location/Qualifiers
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/clone="UUGC1M0164L10"
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of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xi10-Gold (Stratagene) cells and selected for ampicillin resistance."
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TCTGTCACTGCAAACTCACAGTG 55
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979.00
92.82%
89.95%
55.25%
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Best Local Similarity:
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/tissue_type="mix - brain, ovary, placenta, kidney, lung, liver, embryo, heart, muscle, spleen" /lab_host="SOLR"
                                  Euteleostomi;
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Xho1; Estimated insert size approx.1 kb"
165 c 153 g 150 t
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S Lee, N. H., Glodek, A., Chandra, I., Mason, T. M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & R. Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC tel#703-365-2700 for further information
Seq primer: M3 Reverse
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/db_xref="taxon:10116"
/clone="RGIDW31"
/clone_lib="Rat gene index, no
Bento Soares"
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93.97%
55.02%
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-CT0249-120100-022-c03&t3=2000-01-12&t4=1)
Seq primer: puc 18 forward
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1 (bases 1 to 620)

HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project

Oppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
180
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                                        61 AlaGlyGlnHisSerProLeuArgGluGluHisValThrCysValGlnSerIleLeuAsp
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Conservative:
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/db_xref="taxon:9606"
/clone_lib="CT0249"
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High quality sequence stop: 583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                   Homo sapiens
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620 bp mRNA linear EST 23-MAR-2000 RCI-CT0249-290100-022-c03 CT0249 Homo sapiens cDNA, mRNA sequence. AW604359 AW604359.1 GI:7309100
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-CT0249-
290100-022-c03&t3=2000-01-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 583.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 620)
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
                                             329
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GAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGAAG
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                                                                                                                                                                          270 AATGACCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACAGTCCCCTGAAAAGGT
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The FAPESP/LICR Human Cancer Genome Project
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200 ATCCCCATCCACCTGGAGGTGCATTGGTCCCTCATCTGTTGATGTGAGGCGACGCACC
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SmaI; A mini-library was made by cloning products derived
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,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
a 146 c 163 g 150 t
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RCS-BT0604-150200-031-E07 BT0604 Homo sapiens cDNA, mRNA sequence.
BE077141
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High quality sequence stop: 499.

High quality sequence stop: 499.

Location/Qualifiers

1. :572

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//16 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

NT 140 a 143 c 149 g 140 t
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-BT0604-150 200-031-E07&t3=2000-02-15&t4=1)
Seq Primer: puc 18 forward
EUKaryote, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 572)
Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao
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20202663
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Fax: +55-11-2707001
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bp mRNA linear EST 16-FEB-2001 sapiens cDNA clone CS0DK002YD13 3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 626)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
275
                                                                                379
                                                                                                           276 TyrPheLysMetAsnValAlaArgGlnAsnAsnAspSerAspCysGlyAlaPheValLeu 295
                                                                                                                                      380 TACTICAAAAIGAATGIGGCCAGGCAGAATAATGACAGIGACIGIGGTGCTITITGIGIIG 439
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                                                                                                                                                                           440 CAGIACTGCAAGCATCTGGCCCTGTCTCAGCTTCACCTTCACCCAGCAGACATGCCC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                     256 TyrLeuGlnAlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGly
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Matches:
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AL578220
AL578220.1 GI:12942089
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136 GlyPheArgValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyr 155

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BI152305 870 bp mRNA linear EST 05-JUL-2001 602917742F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5067995 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="IMAGE:5067995"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Paraged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
found through the I.M.A.G.E. Consortium/LLNL at:
LLAMIIIS Tow: d column: 12
High quality sequence stop: 523.
Location/Qualifiers
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Unpublished (1999)
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/organism="Mus musculus"
/strain="CZECH II"
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Stem cell origin."

//ab_nosta_"0H108"
//note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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## ALIGNMENTS

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; Human polynucleotide SEQ ID NO 628 AAI58425 standard; cDNA; 2080 BP 2000US-0488725. 2000US-0552317. 2000US-0598042. 2000US-0620312. 2000US-0653450. 2000US-0653450. 2000WO-US34263 22-OCT-2001 (first entry) WO200153312-A1. 21-JAN-2000; 25-APR-2000; 209-JUL-2000; 219-JUL-2000; 203-AUG-2000; 214-SEP-2000; 219-OCT-2000; 2 Leukaemia; ss Homo sapiens. 26-DEC-2000; 26-JUL-2001 AAI58425; RESULT 1 AAI58425 Human polynuciecti Human fetal brain Human polynuclecti Human polynuclecti secreted pro ovarian anti secreted pro

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AAE54831 AAI58426 AAZ43782 AAI60211 AAI60212 AAD05502 ABQ54216 AAD05541

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                                                                                                                                                                                                                                                                                           Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
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1653 AAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAACTCCAGTTCCTTTC 1712 959 1173 IGCATITCTICAATAGTITCTICTATGATAAACTCCGTACCAAGGGTTAIGAIGGGGTGA ACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTATCTACAGGCAG AGGCGGTAAAGAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAAATGA AGATCTACAAGGAGCTGTGTCACTGCAACTCACTGTGTGAGCCTCGTACCCCAGACCCC 573 AGGAAGATGGACTCAGGTGGACTCCAAAGTCTCCTCTGGACCCTGACTCGGGCCTCTTT AGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCAGAGGCCTGGGGGAGA AAGCCGGCCAGCACACCCCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGG ACGAATTCCTTCAAACGTATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGA AGCTGGAGGACATTTTCCAGCAGGAGTTTTCCACCCCTTCCAGGAAGGGCCTGGTGTTGC AGCTGATCCAGTCTTACCAGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCCGAGTGG CTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGC TCAATGACCAGGTGATGAACATGTATGGAGACCTGGTCATGGACACAGTCCCTGAAAAGG TGCATTTCTTCAATAGTTTCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGTGA AAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCTAATCCCCCATCCACC TGGAGGTGCATTGGTCCCTCATCTCTTTTGATGTGAGGCGACGCACCATCACCTATTTTG ATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGCAAGC AGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCGTACCCCAGACCCC AAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAACTCCAGTTCCTTTC CACCCCCTGATGCCAGCATCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCC AGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCCAGAGAGGCCTGGGGAGA 1053 1113 1140 1233 1200 1293 1260 1353 1413 1380 541 633 693 753 813 780 873 840 933 993 1020 1320 1473 1440 1533 1500 009 099 720 006 096 1080 q

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The present sequence encodes a human de-sentrinase (SENP) 3 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                    SENP; SENP1; SENP2; SENP3; chromosome 12q13.1;
                                                                                                                                                                                                                                                                                                                                                                                                            sentrin-specific protease; sentrin; anti-proliferative agent;
anti-viral agent; herpes simplex-1; cytomegalovirus; sentrinisation;
PML; tumour suppressor; acute promyelocytic leukaemia; ss.
          GAAAAGCCCCTTTCTTCTTCTTTGCAGGGGAGTGTGGCCCTGTGGCCTGGGTGGAGCA
                                                                                                                                                                                                                 CTCTCTTGCCTCTTCCCACTCCCTTTGGTTTTTCATATTTAAATGTTTCAATTTC
                                                                                                  1833 GAAAAGCCCCTTTCTTCCTCTGTTTGCAGGGGAGTGTGGCCCTGTGGCTGGGTGGAGCA
                                                                                                                       GTCATCCTCCCCCTTCCCCGTGCAGGAGCAGGAAATCAGTGCTGGGGGGTGGTGGCGGGA
                                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding de-sentrinase polypeptides,
                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a human SENP2 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                    de-sentrinase;
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P-PSDB; AAB31977.
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The specification describes SENP1 and SENP2 polypeptides. The SENP1 gene is found in chromosome 12q13.1. SENP1 is found in the nucleolus, SENP3 is found in the nucleolus, and SENP3 is found in both locations. SENP polypeptides are sentron-specific proteases that remove sentrin from some sentrinised peptides, but do not affect proteins modified by ubiquitin or NEDDB. SENP polypeptides are used to identify specific and anti-viral agents such as herpes simplex-1 or cytomegalovirus. SENP polypeptides are used for studying the role of sentrinisation in the biological function of PML, a tumour suppressor implicated in development of acute promyelocytic leukaemia. Fragments of SENP polynucleotides are used as hybridisation probes and amplification
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Pred. No. 0;
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Best Local Similarity
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
2078 CAATAGGATCACTGCCTGCCAGATCTTCAAACTTT------TATAT 2117
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Yang Y,
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Xu C, Xue AJ,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 629.
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2000US-0552317.
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2000US-0693036.
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19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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AZ43777-Z43808 represent the polynucleotides described in the invention which encode the proteins represented in AAV50905-Y50947.
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                                                                                                                                                                         Human; secreted protein; treatment; nutritional activity; cytokine; cell proliferation; cell prosibilitation; hematopolesis regulation; tissue growth; activin; inhibh; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted human proteins, derived from human fetal brain, adult skin, adult brain, adult heart, adult thymus and adult aorta cDNA libraries.
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03-AUG-2000;
14-SEP-2000;
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29-NOV-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as lazhedimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, cutilisation of the activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and who was a disorders.
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        Wang D;
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  Ren F,
Zhang J
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Yang Y,
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  ien R, Ma Y, (
u C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                   nucleic acids and polypeptides, useful as central nervous system injuries -
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0; Mismatches
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     Chen R,
Xu C, )
Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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Best Local Similarity 97.1%;
Matches 1719; Conservative
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P-PSDB; AAM41055.
                                                     Zhou P,
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           CATCTTGGACGAATTCCTTCAAAC-GTATGGCAGCCTCATACCCCTCAGCACTGAGG
                                                TCCGAGTGGCTTATAAGCGGCACGTGCTGACCATGGATGACTTGGGGACCTTGTATGGAC
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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Goodrich R,
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2000US-0598042.
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Wang Z, Wehrman T,
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19-JUL-2000;
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Wang J, V
Zhao QA,
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        of
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        part
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                             T; 0 other;
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        not
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        did
                                           Score 1568.2;
Pred. No. 0;
0; Mismatches
                              468 G; 428
        patent
       this
                              ပ်
                              431 A; 477
                                           Query Match 78.8%;
Best Local Similarity 97.1%;
Matches 1719; Conservative
       for
       data
C.N.S disorders.
Note: The sequence
                              BP;
                             Sequence 1804
               specification
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                                                1308
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           ACTTCGTCGCCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTGTGAGCCTCGTA
                                                                                                                                                                                                                                                                  GCAGGGGGGGGCTACAG-AAAAGCCCCTTTCTTCTTCTTGTTT----GCAGGGGAGTGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACCTATTTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTA
                                                                                                  TCTACAGGCAGAGGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTA
                                                                                                                                                    CTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTTGCA
                                                                                                                                                                                                    GTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAA
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24;

Indels

Mismatches 178;

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Conservative

Matches 1672;

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neurological disorder; Alzheimer's disease; food additive;
                                                                                                                                           Olsen HS,
                                                                                                                                                                                 Claim 1; Page 417-418; 540pp; English
                                      Location/Qualifiers
                                                                                                                                           Shi Y,
                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                         01-NOV-2000; 2000WO-US30036
                                                                                                                   05-NOV-1999; 99US-0163576.
27-JUL-2000; 2000US-0221366.
                                                                                                                                           Soppet DR, Komatsoulis G,
                                                    /product= 441..521
                                                              /*tag- b
522..710
                                           441..713
/*tag= 8
                                                                        /*tag=
                                                                                                                                                    WPI; 2001-316492/33.
                   therapy; ss.
                                                                                                                                                         P-PSDB; AAE01682
                                                                                       WO200134767-A2
inflammation;
                            Homo sapiens
                                                         sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMOUS 492-AAD05564 represent cDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the proteins they encode.

AAE0174 AAE01763 represent human secreted protein fragments or variants.

CC The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 22 genes, based on the itssues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, the diagnosis or treatment of proliferative disorders, diseases of the immune system AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, diabetes, asthman, skin disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitative disorders, schizophrenia, asthma, skin disorders, and indiabetes, and crimed isorders, and indications. The proteins can also be used to aid wound healing and epithalial cell proteins can also be used to aid wound healing and epithalial cell proteins can also be used to aid wound healing and epithalial coll partners, and in chemotaxis, and can be used as a food additive or professor of modify storage properties. Antibodies specific for a professor of the invention can be used in alleviating symptons associated
angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
The present sequence represents a human secreted protein-encoding cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                      "Human secreted protein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM;
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DB 22; Length 1934;

Score 1451.2; Pred. No. 0;

72.9%; 89.2%;

Best Local Similarity

Query Match

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1135
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Gaps
                                    GAGGAGGAGGAGGATGAAGATGAAGAGGAGGAGGAAGTGGCAGCTTGGAGGCTGCCCCCA 116
                                                                                                        AGATGGAGTCAGCTGGGAACCTCCCAGCGGCCCCGCCCTTCCCGCCCCCACTCATCGAAAA 176
                                                                                                                          132 ACCTGCTCCCAGCGCCGCCGCCGAGCCATGAGGCCTTCCGGATGCTGCTGTACTCGAAA 191
                                                                     71
                                                                     12 GAAGAGGAGGATGAGGATGAGGAAGAGGAAGTGGCAGCTTGGAGGCTGCCCCCC
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Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
ovarian cancer; breast cancer; tumour; reproductive system disorder;
infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
inflammatory condition; immune disorder; blood disorder;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polyucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen.

CC recombinant vectors and host cells comprising human ovarian antigen of ovarian antigens and present of ovarian polyuncleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, copylyostic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), chlood-related disorders (e.g., anaemia), cardiovascular disorders, and urinary system disorders, neurological disorders, gastrointestinal disorders and urinary system disorders, ovarian antigen polypeptides and collabore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    further be used for game therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the obypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, dury targeting and phenotyping. The present sequence represents cDNA encoding a human ovarian antigen of the
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neurological disorder;
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                     gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; fortensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
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    cardiovascular disorder; respiratory disorder;
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NO: 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein-encoding gene 11 cDNA clone HOFOB27, SEQ ID
             1450 CGGCAGATCTACAAGGAGCTGTGTGTCACTGCAAACTCACTGTGTGAGCGTCGTATCCCAGG
                                                                                                                                                                                                                                                                                                        TITGACTCGCAGCGTACCCTAAACCGCCGCTGCCCTAAGCATATTGCCAAGTATCTACAG
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                                                         GCAGAGGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAAA
                                                                                                                ATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGCAGTACTGC
                                                                                                                                                                          <u> AAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGT</u>
                                                                                                                                                                                                                                                                                         CCCCAAGCCCA----TAAATGGGAAGGGAGACATGGGAG----TCCCTTCCCAAGAAACT
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AAD05541 :
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ADD05492-AAD05564 represent CDNAs corresponding to 22 human secreted protein genes, and AAE01672-AAE01743 represent the protein stagements of protein fragments or variants. AAE01744-AAE016762 represent human secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted protein in a manner of the protein or gene therapy. Pathological conditions can be diagnosed by determining the presence of amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the can include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of abordars, endies and include developing products for the diagnosis or treatment of abordars, and include developing products for the diagnosis or treatment of abordars, and include developing products (e.g., Alzheimer's disease, Albs, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Sthan disorders, and infections. The proteins can also be used to aid wound the allow of an anintain organs before transplantation, for supporting cell culture of primary tissues, to respendent tissues, to identify their contact ligands or binding partners, and in chemotaxis, and can be used to a protein of the invention of the prodict of a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassavs e.g., radioimmunoassay or enzyme linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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immunosorbent assay (ELISA). The present sequence represents a
                                                                             /product= "Human secreted protein precursor"
                                                                                                                                                                                                                      /product= "Mature human secreted protein"
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27-JUL-2000; 2000US-0221366.
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Ger. 29, 53, 68.28; Score 1357.4; DB 22; Length 1507;

Best Local Similarity 98.58; Pred. No. 2e-308;

Matches 1358; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
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AGCAGGAGTTYTCYACMCCTTCCAGGAAGGGCCTGGTGYTGCAGCTGATCCAGTCKTACC 1108 1158 IGGACATCTTCAATAAGGAGCTACTGCTAATCCCCCATCCACCTGGAGGTGCATTGGTCCC 1217 TGACCATGGATGACTTGGGGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGATGA 1037 ACATGTATGGAGACCTGGTCATGGACACAGTCCCTGAAAAGGTGCATTTCTTCAATAGTT 1097 TCTTCTATGATAAACTCCGTACCAAGGGTTATGATGGGGTGAAAAGGTGGACCAAAAACG 1157 ATGACAGTGACTGTGGTGTTTTGTGTTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGC 1457 CATTCAGCTTCACCCAGCAGGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGT 1517 GTCACTGCAAACTCACTGTGTGAGCCTCGTACCCCAGACCCCAAGCCCATAAATGGGAAG 1577 GGAGACATGGGAGTCCCTTCCCAAGAAACTCCAGTTCCTTTCCTCTTTGCCTCTTCCCA 1637 CICACITCCCTITGGILTITCATAITTAAAIGITTCAATITCIGIATTITTTTTTTTTG 1697 208 737 808 388 GGAGACATGGGGAGTCCCTTCCCAAGAAACTCCAGTTCCTTTCCTCTCTTGCTCTTCCCA 618 TCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGCCCCAGGAGCTTTTTCAGGGCT 1407 TCCTCATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCT CAGATTTGGGCATGGCAGAGGCAGAGGCCTGGGGAGAAAGCCGGCCAGCACAGCC CCCTGCGAGGGGGGCATGTGACCTGCGTACAGAGCATCTTGGACGAATTCCTTCAAACGT CCCTGCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGGACGAATTCCTTCAAACGT ATGGCAGCCTCATACCCCTCAGCACTGATGAGGTAGTAGAGAAGCTGGAGGACATTTTCC ACCAGGAGTTTTCCACCCCTTCCAGGAAGGGCCTGGTGTTGCAGCTGATCCAGTCTTACC AGCGGATGCCAGGCAATGCCATGGTGAGGGGCTTCCGAGTGGCTTATAAGCGGCACGTGC 347 1287 1167 1218 687 1398 627 1107 1038 8601 1458 1518 678 738 798 918 978 887 867 807 267 507 447 387 g ò q ò g ò g Ω 엄 δ qq ŏ g δ Д δ g δ Ω ò g ò g οy οp δý q g ò 셤 a

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                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial; gene therapy; detection; cancer; chromosome marker; chromosome identification; neural disorder; immune disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; profilerative disorder; wound healing; infectious disease; preservative;
AGAGAATACTTGTTGATTTCTGATGTGCAGGGGGTGGCTACAGAAAAGCCCCTTTCTTCC 1757
                                                TCTGTTTGCAGGGGAGTGTGGCCCTGTGGCTGGGTGGAGCAGTCATCCTCCCCCTTCCC 1817
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                                                             Human secreted proteins and gene sequences encoding them, useful for detecting, preventing, and treating disorders such as cancer, neurological disorders and immune system disorders -
             Human secreted protein gene 4 SEQ ID NO:14.
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                                                          also be used as a food additive or preservative to increase or decrease storage capabilities. AAC59557 to AAC59565 and AAB34298 represent
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                                                                                                                     sequences used in the exemplification of the present invention
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                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AbD05492-AbD05564 represent cDNAs corresponding to 22 human secreted protein genes, and AbE01672-AAE01743 represent the protein stage encode. ABE01744-ABE01763 represent human secreted proteins show their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted proteins and their genes are useful for preventing. The secreted protein is and their genes are useful for preventing. The secreted protein in a sample or by determining the presence of mount of the new protein in a sample or by determining the presence of another of the new genes. Specific uses are described for each of the 22 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, DIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, cardiovascular disorders, angiogenic disorders, kidney disorders, and infections. The proteins can also be used to aid wound healthing and epithelial cell proliferation, to prevent skin aging due to subtract the contract of an example of the subtraction of an example of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of the subtraction of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
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                                                                                                                                                               'product= "Human secreted protein precursor"
                                                                                                                                                                                                                                                                     /product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olsen HS, Ruben SM;
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cell culture; chemotaxis; food additive; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 446-447; 540pp; English.
                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2000; 2000WO-US30036.
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27-JUL-2000; 2000US-0221366.
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159..164
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                                                               Homo sapiens
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                                                                                                                                                                                    sig_peptide
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Human; eukaryotic transcription factor 4A; eIF4Al; promoter;
DNA construct; DNA vaccine; gene therapy; cancer; Parkinson's disease;
cystic fibrosis; hepatitis; HIV; ds.
                                                              AGATGGGGTCAGCTGGGAGCTTCCCAGCGGCCTCGTCCTCCCCGCCCTACTCATCGAAAA 136
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GAAGAGGAGGATGAAGATGAAGAAGAAGAAGTGGCAGCTTGGAGGCTGCCCCCC 76
                                                                                                               376 GGTGCTCTCATGGCTGAGGATGGGATGAGAGGGTCTCCACCGATGTCCTCTGGGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGCTCACAGGGCCGCCGCCGAGCCATGAGAGCCTTCCGGATGCTGCTCTACTCAAAA
                                                                                                                                                              AGCACCTCGCTGACATTCCACTGGAAGCTTTGGGGGGGCGCCACCGGGGGCCGGCGGGGGGG
                                                                                                                                                                                                                              CTCGCACACCCCAAGAACCATCTTTCACCCCAGCAAGGGGGGTGCGACGCCACAGGTGCCA
                                                                                                                                                                                                                                                                                           TCCCCCTGTTGTCGTTTTTGACTCCCCCCGGGGGCCACCTCCACCCCGGGTTGGGTCTGCTA
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14-DEC-1999;
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Gaps

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Best\_Local Similarity 90.2 Matches 617; Conservative

(first entry)

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Human;
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                                                                                                                  The present invention describes a DNA construct comprising a transcriptional regulatory sequence linked to the gene of interest wher the regulatory sequence linked human enkaryotic initiation factor 4A1 (eIF4A1) gene promoter. This can be used in the production of DNA vaccines and gene therapy, both of which can be used in the prevention and treatment of diseases such as cystic fibrosis, parkinson's disease, cancer, hepatitis B and C, HIV, tuberculosis, HPV, HSV, multiple sclerosis, Alzheimer's disease and asthmal It can also be used in
                                                                                                                                                                                                                                                                                1427 CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAGGACATGCCC 1486
                                                                                                                                                                                                                                                                                          3827 CAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCTAGCAGCAGACATGCCC 3886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4366
                                                          New DNA constructs, useful in gene therapy for treating or preventing chronic inflammatory reactions such as multiple sclerosis or asthma, a DNA vaccines, or in the commercial production of proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5318;
                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                      Sequence 5318 BP; 1327 A; 1210 C; 1423 G; 1350 T; 8 other;
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                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                  Score 486.4; DB 22;
Pred. No. 7.6e-104;
                                                                                                                                                                                                    vaccines for contraception or drug addiction.
                    Ford
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                    Catchpole IR,
                                                                                                 Claim 19; Page 58-62; 62pp; English
                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 94.9%;
Matches 544; Conservative
                    'n
(GLAX ) GLAXO GROUP LTD
                                      WPI; 2001-138151/14
                    DR,
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standard; cDNA; 870

AAI94288

AAI94288/C

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The invention relates to novel genes (AA193926-AA197963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy as usceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids originating in gene expressed in human neuroblastoma useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour mafor anti-cancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   519 GACCCTGACTCGGGCCTCCTTTCATGTACTCTGCCCAACGGTTTTGGGGGACAATCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579 -CCAGAAGGGGAGCGCACTTGGCACCCCC-TGATGCCAGCATCCTCATCAGCAATGTGTG
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                                                     neuroblastoma; malignancy; cancer; tumour marker; N-myc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 870;
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Human neuroblastoma expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 870 BP; 217 A; 229 C; 190 G; 211 T; 23 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.5%; Score 468.4; DB 22; Best Local Similarity 94.3%; Pred. No. 5.9e-100; Matches 533; Conservative 0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 308-309; 2979pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for N-myc and TrkA genes
                                                                                                                                                                                                                                                                                                                                                                                                       (CHIB-) CHIBA PREFECTURE.
(HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                               07-MAR-2000; 2000JP-0159195.
                                                                                                                                                                                                                                                                                      02-MAR-2001; 2001WO-JP01629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-565584/63.
                                                                                                                                                                       WO200166719-A1.
                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawara A;
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503 ACTCCGTACCAAGGGTTATGATGGGGTGAAAAGGTGGACCAAAAACGTGGACATCTTCAA 444

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ovarian cancer. The compositions comprise one or more ovarian tumour toboteins, their associated polynucleotides, or immunogenic portions of the proteins. The ovarian tumour polynucleotides and polypeptides are useful for stimulating and/or expanding T cells specific for a tumour protein. They are also useful for inhibiting the development of cancer in protein. They are also useful for inhibiting the development of cancer in a patient with an ovarian tumour DNA or protein by incubating isolated T-cells allowing them to proliferate, for cancer, for example, to monitor ovarian cancer progression. Probes and primers are useful in nucleic acid hybridisation, in detecting the presence of complementary sequences in a given sample, for preparing mutual species and for preparing other genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises compositions used for the therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                       Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss; gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides encoding ovarian tumour proteins, useful for uting ovarian cancer, and as probes, primers, and markers of cancer
                                                           GGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGATGAACATGTATGGAGACCTGG 1055
CCATGGTGAGGGGCTTCCGAGTGGCTTATAAGCGGCACGTGCTGACCATGGATGACTTGG 995
                 Score 442; DB 22; Length 503;
Pred. No. 7.3e-94;
0; Mismatches 0; Indels 51
                                                                                                                                                                                                                                                                                                                          Human ovarian PCR-subtracted cDNA library clone #1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 503 BP; 120 A; 110 C; 147 G; 126 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent human ovarian tumour protein cDNA clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; page 375; 378pp; English
                                                                                                                       1056 TCATGGACACAGTCCCTGAAAAGGT 1080
                                                                                                                                       331 TCATGGACACAGTCCCTGAAAAGGT 307
                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                 AAS25529 standard; cDNA; 503
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ilarity 90.8%;
Conservative
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28-MAR-2000; 2000US-0192745.
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                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Algate PA, Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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hes 503; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                        primer; probe.
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 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1530
                                                                                                                                                                                                                                                                                    1351 CCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTG 1410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1411 TGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTGTGTGAGCCTCGTACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAG 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -------GTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75
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TGTGAGGCGACGCACCATCACCTATTTTGACTCGCAGCGTACCCTAAACCGCCGCTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1471 CCAGCAGGACATGCCCAAACTTCGTCGGCAGATCTACAAGGAGCTGTGTCACTGCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 CCAGCAGGACATGCCCCAAACTTCGTCGCGCAGATCTACAAGGAGCTGTGTGTCACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neuroblastoma expressed polynucleotide SEQ ID NO 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI93958 standard; cDNA; 820
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                            The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnoshing prognosis is related to factors similar to that for N-myc and TrkA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      996 GGACCTTGTATGGACAGAACTGGCTCAATGACCAGGTGATGAACATGTATGGAGACCTGG 1055
                                                                                                                                                                                                                                                                                                                                                                            CAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGA 696
                                                                                                                                                                                                                                                                                                                                                                                             756
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                                                                                                                                                                                                                                            517 TGGACCCTGACTCGGGCCTCCTTTCATGTACTCTGCCCAACGGTTTTGGGGGGACAATCTG 576
                                                                                                                                                                                                                                                              577 GCCCAGAAGGGGAGCGCACTTGGCACCCCTGATGCCAGCATCCTCATCAGCAATGTGTG 636
                                                                                                                                                                                                                                                                                                                           649 A---GCAGAGAGCCTTGGGGAG-AAGCCGGCAGAACAGCCCCTTGNGAGAGGAGCATGT 594
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                                                                                                                                                                                                                 14;
                                                                                                                                                                             DB 22; Length 820;
                                                                                                                                                                            Score 362.2; DB 22; Length
Pred. No. 4.7e-75;
0; Mismatches 70; Indels
                                                                                                                                             Sequence 820 BP; 224 A; 223 C; 170 G; 191 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1056 TCATGGACACAGTCCCTGAAAAGGT 1080
Claim 1; Page 59; 2979pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.2%;
Best Local Similarity 85.1%;
Matches 481; Conservative
                                                                                                                                                                                                                                                                                                                                                                          637
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Search completed: December 16, 2002, 15:38:59 Job time: 418 secs

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Sequence 79, A Sequence 7, Ap Sequence 7, Ap Sequence 18, A
                   Sequence Sequence Sequence S
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Sequence
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Sequence
Sequence
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Sequence
Sequence
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APPLICANT: Kaloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Millian, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
MINMER OF SEQUENCES: 5
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATCHLIN RELEASE #1.0, VETSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
TELING APPLICATION NUMBER: PCT/US97/18802
FILING APPLICATION NUMBER: 05-OCT-1997
PRIOR APPLICATION NUMBER: 05-OCT-1997
FILING DATE: 00-OCT-1997
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
               US-07-799-828C-8
US-08-074-275-8
US-08-07-952-277A-8
US-07-91-211-3
US-08-791-211-3
US-08-207-904-18
US-09-207-904-18
US-09-791-79
US-09-791-79
US-09-791-79
US-09-791-79
US-09-791-79
US-09-724-394A-21
US-08-724-394A-21
US-09-72-317-55
US-09-604-838-89
US-09-622-217-55
US-09-622-217-55
US-09-604-838-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 51952 base pairs;
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
128
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87350
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ZIP: 94111-3834
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APPLICANT: Willia
   COUNTRY:
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Patent No. 5312912
Sequence 4, Appli
Sequence 1, Appli
Sequence 17, Appli
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9540.522 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Al Sequence 8, Al Sequence 8, Al Sequence 8, Al Sequence 17, Sequence 17,
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1991
1 GCCTCCCTGTCCCCGACCC.....TGCTCTGGTCAATAAAGATC 1991
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                                                                                                                                 December 16, 2002, 13:18:49; Search time 64 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-08-616-368A-17
US-09-054-298-17
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-08-616-368A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-922-723A-8
US-07-799-828C-8
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US-09-433-579-3
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-08-818-655-17
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-08-480-366-8
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US-08-550-544-4
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                                                                                                                                                                                                                                                                                                                                             441362 segs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapox 10.0
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence:
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No.
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GENERAL INFORMATION:

APPLICANT: Cramer, Carole L.

APPLICANT: Cramer, Deborah L.

APPLICANT: Weissenborn, Deborah L.

TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM AND

TITLE OF INVENTION: POST-HARVEST PRODUCTION OF GENE PRODUCTS

TITLE OF INVENTION: IN PLANTS AND PLANT CELL CULTURES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,581
FILING DATE: 29-JUL-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08282581 Patent No. 5670349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oy 1942 ATATATATAAATATAAAT 1961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 75
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 90.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 480 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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US-08-282-581-4/c
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                                                                                                                               Gaps
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APPLICANT: Williamson, Valerie M.
APPLICANT: Raloshian, Isgouhi
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Bodeau, John
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.4%; Score 67.8; DB 6; Length 1890; Best Local Similarity 78.6%; Pred. No. 4.8e-08; Matches 81; Conservative 0; Mismatches 22; Indels 0
  Length 51952;
                                                                                                                                                                                                                                                                                                                                                                                        FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER INDUCIBLE TRAITS IN PLANTS

NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DAIR:

APPLICATION DAIR:

FILING DAIE: 13-JUN-1989
                                           20; Indels
                                                                                                                                                                                                   Db 13725 ATATATATATATATATATATATTATTCTTATAAAAAAA 13766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1919 TATATATATATATATATATATATATATATAAAATATATAAAT 1961
                                                                                                                                                                                                                                                                                                                           Fatent No. 5312912;
APPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ,
                                                                                                                                                                          1948 ATAAATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGA 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Townsend and Townsend and Crew LLP
F: Two Embarcadero Center, Eighth Floor
San Francisco
California
Score 70; DB 3; 1
Pred. No. 6.6e-08;
0; Mismatches 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-947-823-1/c
; Sequence 1, Application US/08947823
; Patent No. 6114605
Query Match 3.5%;
Best Local Similarity 80.4%;
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:3
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                                                                                                                                                                                                                                                                                                         5312912-3
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         FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
PCT/US97/18802
APPLICATION NUMBER:
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5312912-3/c
;Patent No. 5312912
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   LOCATION:
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                                                                                                  LOCATION
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US-08-282-581-4
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STATE:
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                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                     Length 480;
                                                                                          LOCATION: 162
OTHER INFORMATION: /label- n
OTHER INFORMATION: /note- "n=x=Unknown nucleotide"
                                                                                                                                                                                                ; OTHER INFORMATION: /label= n; OTHER INFORMATION: /note= "n=x=Unknown nucleotide" US-08-282-581-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cramer, Carole L.
APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               1952 ATATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGAT 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATATATATATGCAGAAGTATCTTTGTAGATTATAAT 207
                                                                                                                                                                                                                                                                             3.4%; Score 67; DB 1; 79.8%; Pred. No. 3.9e-08; Live 0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,816
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7956-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/550,544 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08550544 Patent No. 5689056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                   NAME/KEY: modified_base
                                                                         NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                               Query Match 3.4 Best Local Similarity 79.8 Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-550-544-4/C
                                                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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Patent No. 5670349
GENERAL INFORMATION:
APPLICANT: Cramer, Carole L.
APPLICANT: Welssenborn, Deborah L.
TITLE OF INVENTION: HAG2 PROMOTER EXPRESSION SYSTEM AND
TITLE OF INVENTION: POST-HARVEST PRODUCTION OF GENE PRODUCTS
TITLE OF INVENTION: IN PLANTS AND PLANT CELL CULTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES; FOR GENETICALLY ENGINEERING DISEASE RESISTANCE AND OTHER INDUCTBLE TRAITS IN PLANTS; NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
PILING DATE: 13-JUN-1989
                                                                                                                                                                                       Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1948 ATAAATATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGAT 1990
                   /note= "n=x=Unknown nucleotide"
                                                                                                       /label= n
/note= "n=x=Unknown nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 ATATATATATATAACAACTCAATATCTCTGTCATAATTAT 156
                                                                                                                                                                                                                                                                                                                                                                 1952 ATATATAAATGCCACGGTCCTGCTCTGGTCAATAAAGAT 1990
                                                                                                                                                                                                                                                                                                                                                                                            245 ATATATATATATGCAGAAGTATCTTTGTAGATTATAAT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.3%; Score 66.2; DB 6; Best Local Similarity 77.7%; Pred. No. 1.2e-07; Matches 80; Conservative 0; Mismatches 23;
                                                                                                                                                                                       Score 67; DB 1;
Pred. No. 3.9e-08;
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS
STREET: 1155 Avenue of the Americas
CITY: New York
  /label= n
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                         3.4%;
                                                             NAME/KEY: modified_base
                                                                                                                                                                                                                                 79; Conservative
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                     OTHER INFORMATION:
COTHER INFORMATION:
US-08-550-544-4
                                                                                                                                                                                         Query Match
Best Local Similarity
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Query Match 3.3%; Score 65.8; DB 1; Length 480; Best Local Similarity 90.9%; Pred. No. 8e-08; Matches 70; Conservative 0; Mismatches 7; Indels
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Patent No. 5767262
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
CORRESPONDENCE: 1518 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /label= n
OTHER INFORMATION: /note= "n=x=Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= n
/note= "n=x=Unknown nucleotide'
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ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION UNBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/022001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1996
                                                                             7956-004
                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 base pairs
TYRE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                            18872
                  ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 188
REFERENCE/DOCKET NUMBER:
02-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                           1944 ATATATAATATATAA 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified_base LOCATION: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 225 F1
CITY: Boston
STATE: MA
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US-08-616-368A-17
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          SOFTWARENT STATEM.
SOFTWARENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,581
FILING DATE: 29-JUL-1994
CLASSIFICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: MASTOCK; S. Leslie
REGISTRATION NUMBER: 18872
REFERENCE/DOCKET NUMBER: 18872
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ. 10 NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 162
OTHER INFORMATION: /label- n
OTHER INFORMATION: /note= "n-x-Unknown nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 356

COTHER INFORMATION: /label= n

OTHER INFORMATION: /note= "n=x=Unknown nucleotide"

US-08-282-581-6
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APPLICANT: Cramer, Carole L.
APPLICANT: Weissenborn, Deborah L.
TITLE OF INVENTION: HMG2 PROMOTER EXPRESSION SYSTEM
TUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,816
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-550-544-4
; Sequence 4, Application US/08550544
; Patent No. 5689056
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1944 ATATATAAATATAAA 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified_base LOCATION: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base
LOCATION: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 480 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.3'
Best Local Similarity 90.9'
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036-2711
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   9; Indels
                                                                                                                                                                                                                                                                                        APPLICANT: Lee, Mu-En
APPLICANT: Lee, Mu-En
APPLICANT: Jain, Mukesh
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TILE OF INVENTYON: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows95
SOFTWARE: Fast5ED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,655
FILING DATE: 14-MAR-1997
CLASSIFICATION T. 514
PRIOR APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 05433/030001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                 E: Fish & Richardson, P.C.
225 Franklin Street
                                                                                                                                                                                                                                    Sequence 17, Application US/08818655 Patent No. 6258557
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                                                                                                                              267 ATATATATATATACAAAA 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LECTION 297 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71; Conservative
     71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boston
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TOPOLOGY: lir
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STREET: 22
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US-09-433-579-3/c
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   Matches
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                                                                                                                                                                                                                Score 65.6; DB 1; Length 297;
Pred. No. 7.1e-08;
0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edgar
APPLICANT: Jain, Mukesh
APPLICANT: Jain, Mukesh
APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCHEVIEN: 150 COMPUTATION
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows version 2.0b
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/616,368
FILING DATE: 15-MAR-1996
ATTORNEY-AGENT INFORMATION:
NAME: Beattie, Ph.D., Ingrid A.
REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65.6; DB 3;
Pred. No. 7.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09054298 Patent No. 6136953
                                                                                                                                                                                                                                                                                                                                                             1940 ATATATATATATATA 1959
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                                                                                                                                                                                                                 3.3%;
88.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                               TELEX: 200154

INFORMATION FOR SEQ ID NO: 1'S SEQUENCE CHARACTERISTICS:

LENGTH: 297 base pairs:

TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear

MOLECULE TYPE: DNA
US-08-616-368A-17
617/542-5070
617/542-8906
                                                                                                                                                                                                        Ouery Match
Best Local Similarity 88.88
Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-054-298-17
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Length 128;
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                                                                                                                                                                                                                                                                 APPLICANT: Drs. Carl R. Merril and APPLICANT: Mihael H. Polymeropoulos TITLE OF INVENTION: TWENTY SEVEN HIGHLY INFORMATIVE TITLE OF INVENTION: MICROSATELLITE REPEAT TITLE OF INVENTION: POLYMORPHIC DNA MARKERS NUMBER OF SEQUENCES: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08074275
Patent No. 5468610
GENERAL INFORMATION:
APPLICANT: DIS. CARI R. Merril and
APPLICANT: Minael H. Polymeropoulos
TITLE OF INVENTION: THREE HIGHLY INFORMATIVE REPEAT
TITLE OF INVENTION: POLYMORPHIC DNA MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.2%; Score 64.6; DB 1;
80.0%; Pred. No. 8.6e-08;
tive 0; Mismatches 19;
                                                                           1931 TATATATATATATATATATAAATATAAATGCCA 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1931 TATATATATATATATATAAATATATAAATGCCA 1965
                                                                                               STREET: Suite 300, 99 Canal Center Plaza CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/799,828C
FILING DATE: 19911127
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           Sequence 8, Application US/07799828C Patent No. 5378602 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: D.J. Mills
REGISTRATION NUMBER: 34,506
REFERENCE/DOCKET NUMBER: 71706
REFERENCE/DOCKET 7706
TELECOMMUNICATION INFORMATION:
TELEHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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ADDRESSE: Lowe, Pri
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Best Local Similarity
Matches 76; Conserv
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CLASSIFICATION:
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US-07-799-828C-8/C
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APPLICANT: and Carl R. Merril
TITLE OF INVENTION: FIVE HIGHLY INFORMATIVE
TITLE OF INVENTION: REPEAT POLYMORPHIC DNA MARKERS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe, Price, Leblanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%; Score 64.6; DB 1;
80.0%; Pred. No. 8.6e-08;
tive 0; Mismatches 19;
                                                                                                                                                                                                                                                                                     Score 65; DB 4;
Pred. No. 7.8e-07;
0; Mismatches 15
             GENERAL INFORMATION:
APPLICANT: ROTEMANN, William H.
TITLE OF INVENTION: LSAG Gene
CURRENT APPLICATION NUMBER: US/09/433,579
CURRENT APPLICATION NUMBER: US/09/433,579
NUMBER OF SEQ ID NOS: 36
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 3
LENGTH: 17656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 11885 ATATATATACATATATCGAGAGAGA 11857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: D.J. Mills
REGISTRATION NUMBER: 34506
REFERENCE/DOCKET NUMBER: 717081B
TELECHOMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/07922723A Patent No. 5369004 GENERAL INFORMATION:
                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Liquidambar styraciflua
US-09-433-579-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-07-922-723A-8
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Best Local Similarity 83.1%;
Matches 74; Conservative
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Best Local Similarity 80.0°
Matches 76; Conservative
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US-07-922-723A-8/c
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CORRESONDENCE ADDRESS:
ADDRESSE: Lowe, Price Leblanc & Becker
STREET: Suite 300, 99 canal Center Plaza
CTTY: Alexandria
STATE: Virginia
CCOUNTRY: USE 12314
COMPUTER: Windinia
COUNTRY: USE 120PD disk
MUDIUM TYE: PloPPy disk
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1: /cgn2_6/ptodatu3//Pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodatu3//Pubpna/PCT_NRW_PUB.seq:*
3: /cgn2_6/ptodatu3//Pubpna/USO6_NEW_PUB.seq:*
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7: /cgn2_6/ptodatu3//Pubpna/USO8_NEW_PUB.seq:*
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14: /cgn2_6/ptodatu3//Pubpna/USO0_NEW_PUB.seq:*
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Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355320 seqs, 197730502 residues
                                                       version 5 - 2002 C
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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length: 2000000000
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Perfect sc
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 1710, Ap		Sequence 4735, Ap	Sequence 4719, Ap	Sequence 1226, Ap	Sequence 1226, Ap	Sequence 792, App	741, 7		_	182, 7	Sequence 5, Appli	Sequence 1068, Ap	Sequence 82, Appl	1107	Sequence 38, Appl	Sequence 479, App	Sequence 1097, Ap
ΩI	US-09-848-852A-4	US-09-777-564-1710	US-09-983-965-835	US-09-867-701-4735	US-09-867-701-4719	US-09-969-373-1226	US-09-969-373-1226	US-09-969-373-792	US-09-969-373-741	US-09-969-373-780	US-09-969-373-781	US-09-969-373-182	US-09-969-373-5	US-09-969-373-1068	US-09-969-373-82	US-09-969-373-1107	US-09-969-373-38	US-09-910-943-479	US-09-969-373-1097
DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
* Query Match Length DB	1991	503	432	435	106	217	217	138	169	170	242	123	202	229	170	209	144	741	212
% Query Match	100.0	22.2	18.5	4.6	4.3	3.6	3.6	3,5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5	3.5
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## Comparison of the compariso	Sequence 1317, App Sequence 1517, App Sequence 1113, App Sequence 1163, App Sequence 118, App Sequence 118, App Sequence 122, App Sequence 110, App Sequence 110, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 1113, App Seque	Sequence 1068, Ap Sequence 5706, Ap	F SIGNALING
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ive 0; Mismatches
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                                SEQUENCE DESCRIPTION: SEQ-09-848-852A-4
STRANDEDNESS: single
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CLONE: 2056178
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IMMEDIATE SOURCE:
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Best Local Similarity
Matches 1991; Conserv
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Matches 389; Conservative
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                                                                                                                                                                                                                                                                   Score 442; DB 10;
Pred. No. 4.7e-103;
0; Mismatches 0;
                                                  Sequence 1710, Application US/09777564
Fatent No. US200202591A1
GENERAL INFORMATION
FERENCE INFORMATION
FAPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CAN
FILE REFERENCE: 210121.493
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOFTWARE: FastSEQ for Window Version 4.0
ILENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 CCAGGCTGGAAAGGTTACTTCAAAAT---------
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US-09-983-965-835/C
US-09-983-965-835/C
; Sequence 835, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
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1 Similarity 90.8%;
503; Conservative
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CORGANISM: Homo sapiens
US-09-777-564-1710
1981 CAATAAAGATC 1991
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US-09-777-564-1710/c
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 CATCAGCAATGTGTGCAGCATCGGGGACCATGTGGCCCCAGGAGCTTTTTCAGGGCTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGAGAGGAGCATGTGACCTGCGTACAGAGCATCTTGGACGAATTCCTTCAAACGTATGG
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Patent No. US2002013237A1

GENERAL INFORMATION:

APPLICANT: Adjate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 21012.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 29-LIB188-017-Q1:E1-H1 US-09-983-965-835
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Gaps

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Indels

Score 72.6; DB 10; Pred. No. 3.5e-09; 0; Mismatches 19;

Length 217;

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Query Match 3.6%;
Best Local Similarity 81.6%;
Matches 84; Conservative
                ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1226
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US-09-969-373-792/c
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 LENGTH: 217
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                                                                                                                                                                                                                                                                                                                                             Sequence 1226, Application US/09969373
; Sequence 1226, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
    APPLICANT: Effertz, Roger J.
    APPLICANT: Effertz, Roger J.
    TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
    FILE REFERENCE: 38-10(52679)A
; CURRENT FILING DATE: 2001-10-02
    PRIOR PILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-03
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; RIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106;
                                                                                                         Query Match
4.6%; Score 92; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 6.1e-14;
Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 84.8; DB 10;
Pred. No. 1.8e-12;
0; Mismatches 2;
                                                                                                                                                                                                                                     1487 AAACTTCGTCGGCAGATCTACAAGGAGCTGTG 1518
                                                                                                                                                                                                                                                      404 AAACTTCGTCGCCAGATCTACAAGGAGCTGTG 435
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1961 TGCCACGGTCCTGCTCTGGTCAATAAAG 1988
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4.3%;
Best Local Similarity 97.7%;
Matches 86; Conservative (
                                             TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CORGANISM: HOMO sapien
US-09-867-701-4719
                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-867-701-4719/c
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US-09-969-373-1226/c
                                                                             US-09-867-701-4735
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LENGTH: 106
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                                                                                                                   Sequence 792, Application US/09969373
; Sequence 792, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; NUMBER OF SEQ ID NOS: 4593
                        Score 70.8; DB 10;
Pred. No. 1e-08;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1940 ATATATATATATATATATA 1961
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Best Local Similarity 91.5%;
Matches 75; Conservative (
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NUMBER OF SEQ ID NOS: 4593
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US-09-969-373-781
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LENGTH: 242
                      SEQ ID NO 780
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; Sequence 780, Application US/09969373
; Patent No. US20020133822A1
; GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Bilan M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT APPLICATION NUMBER: US 09/754,853
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
; PRIOR FILING DATE: 2001-01-13
                                                                                                        Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INCORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(55679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/756,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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84.9%; Pred. No. 9.8e-09;
                                                                                                      Score 70.6; DB 10;
Pred. No. 8.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1944 ATATATATATATATATGCCACGGTCCTGCTC 1976
                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 741, Application US/09969373 Patent No. US20020133852A1
                                                                                                        3.5%;
                                                                                                                         Best Local Similarity 78.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.9 ses 79; Conservative
                                  ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-792
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CORGANISM: Glycine max
US-09-969-373-741
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US-09-969-373-780
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US-09-969-373-741
SEQ ID NO 792
LENGTH: 138
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LENGTH: 169
                                                                                                          Query Match
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Matches
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                                                                                                              3.5%; Score 70.6; DB 10; Length 170; 81.2%; Pred. No. 9.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 781, Application US/09969373

Sequence 781, Application US/09969373

Patent No. US20020133852A1

GENERAL INFORMATION:

APPLICANT: Effertz.

TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping

TITLE REFERENCE: 38-10(52679)A

CURRENT APPLICATION NUMBER: US/09/969,373

CURRENT FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-05

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

PRIOR FILING DATE: 2001-01-13

NUMBER OF SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Effertz, Roger J.
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR PELLING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-13
PRIOR PLLING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/760,427
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                             1921 TATATATATATATATATATATATATATAAAATATATAAAT 1961
                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                            82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
LENGTH: 170
TYPE: DNA
ORGANISM: Glycine max
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Matches 82; Conserv
                                                                                                                                       Best Local Similarity
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PRIOR APPLICATION NUMBER: US 09/855,768
               PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1668
LENGTH: 229
                                                                                      TYPE: DNA
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                                                                                                                                     Length 123;
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09969373
Fatent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38 10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
SEQ ID NOS: 4593
SEC ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1068, Application US/09969373
; Sequence 1068, Application US/09969373
; GENERAL INCORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TILE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679) S
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR PFILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
; PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                   Indels
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Pred. No. 9.1e-09;
0; Mismatches 21;
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83.3%; Pred. No. 1.2e-08;
tive 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1940 ATATATATATATATATATATGCCACGGTCCTGCT 1975
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ilarity 79.8%;
Conservative
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 182
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80; Conservative
                                                                                                                                                Best_Local Similarity
Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-5
                                                                                 ; ORGANISM: Glycine max US-09-969-373-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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US-09-969-373-5/c
                                                                   TYPE: DNA
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                                                                                                                                    Query Match
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                                                         Length 229;
                                                                                                                                                                                                                                                                                                                                              Sequence 82, Application US/09969373;
Patent No. US20020133852a1
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Effertz, Roger J.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)
CURRENT PELLOG DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/09/969,373
CURRENT APPLICATION NUMBER: US 09/754,853
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR PRILOMION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR SPELICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
SEQ ID NOS: 4593
SES DID NOS: 4593
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                                                       Score 70.4; DB 10;
Pred. No. 1.3e-08;
0; Mismatches 16;
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84.0%; Pred. No. 1.4e-08;
rative 0; Mismatches 15
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                                                         Query Match 3.5%;
Best Local Similarity 83.3%;
Matches 80; Conservative
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Best Local Similarity 84.0%
Matches 79; Conservative
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; ORGANISM: Glycine max
US-09-969-373-82
; ORGANISM: Glycine max US-09-969-373-1068
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US-09-969-373-82/c
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Searched:

Database

Sequence:

Run on:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1071)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1228 row: 1 column: 15
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Location/Qualifiers
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AUTHORS
TITLE
JOURNAL
COMMENT
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VERSION
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BM806659
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BM804530 AGENCOURT
BM806502 AGENCOURT
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BQ440555 AGENCOURT
                                                                                                            (without alignments)
12615.498 Million cell updates/sec
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1 GCCICCCTGICCCCCGACC......IGCICTGGICAATAAAGAIC 1991
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             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                 OM nucleic - nucleic search, using sw model
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Perfect score:
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812.2
805.6
786.4
748.8
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source

. 9 Result

PM3-ET027 AGENCOURT

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bp mRNA linear EST 05-MAR-2002
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THY-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/note="Organ: lymph; Vector: pCMY-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12273 row: i column: 06
High quality sequence stop: 583.
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TITLE
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="limAdE:5548958"
/clone=lib="MIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="MIHO (phage-resistant)"
/note="Coran: skin: Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr
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Pred. No. 3.5e-154;
0; Mismatches 26;
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Best Local Similarity 96.5%;
Matches 947; Conservative
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Homo sapiens cDNA clone IMAGE:5548865
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                             GTTATGATGGGGTGAAAAGGTGGACCAAAAACGTGGACATCTTCAATAA 1173
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AGENCOURT 6542932 NIH_MGC_72
5', mrnA sequence.
BM806502.1 GI:19123325
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TITLE
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COMMENT
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/clone=Lib="NHAGE:5548865"
/clone=Lib="NHAGE:5748867"
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/lab_not="Organ: skin; Vector: pCNV-SPORT6; Site_1: Not1;
/note="Organ: skin; Vector: pCNV-SPORT6; Site_1: Not1;
/organ: ski
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Pred. No. 2.4
Plate: LLAM12258 row: h column
High quality sequence stop: 652.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CsD01013YK06"
/clone=lib="LTI_NFL008_TC2"
/sex="male="T cells from T cell leukemia"
/fissue_type="T cells from T cell leukemia"
/note="Vector: pcMvSPORT 6; Site_1: Not!; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@ilfetech.com URL:
http://fulllength.invitrogen.com"

17 a 199 c 206 g 190 t 5 others
                                                                                                                                                                                                  AL581080 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ013YK06 3 prime, mRNA sequence.
AL581080
AL581080.1 GI:12947725
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1 (bases 1 to 817)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
1282 CCGCTGCCCTAAGCATATTGCCAAGTATCTACAGGCAGA--GGCGGTAAAGAAAGACCGA 1339
                                                          1340 CTGGATTT----CCACCAGGCTGGAAAGGTTACTTCAAAATGAATG--TGGCCAGGCAG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCTGGAGGTGCATTGGTCCCTCATCTCTGTTGATGTGAGGCGACGCACCATCACCTA 1254
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                             839
                                                                         698 CCACCTGGAGGTGCATTGGTCCCTCATCTTGATGTGAGGCGACGCACCATCACCTA 639
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               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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1. .817
                                                                                                                  1394 AATAATGACAGTGACTGTGGTG 1415
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AGENCOURT_6481545 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555330 BM476787
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Catarrhini; Hominidae; Homo.
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1315 GGCAGAGGCGGTAAAGAAGACCGACTGGATTTCCACCAGGGCTGGAAAGGTTACTTCAA 1374
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM12275 row: f column: 03
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 1114)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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AGENCOURT_7827074 NIH_MGC_67 bp mRNA linear EST 24-WAY-2002 57, mRNA sequence.
BQ440555.
EST. GI:21179631
EST.
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 867)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Righ quality sequence stop: 645.

Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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/db.xref="taxon:9606"
/clone="IMAGE:6153067"
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/lab_host="pring (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo (Avcrage insert size 1.75 kb. Library constructed by imenhologies."
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Pred. No. 4.5e-128;
0; Mismatches 10;
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llarity 98.2%;
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Matches
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/clone="IMAGE:5555330"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="BH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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BM555097 GI:18795276
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/db_xref="taxon:9606"
/dboe="InAGE:5737188"
/clone=_lib="NIH_MGC_88"
/clone=lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/tab_host="blide (phage-resistant):
/note="Organ: small intestine; Vector: pCMV-SPORTE;
Site_1: Not!; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

58 c 295 g 272 t a lothers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1099)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can laterize LLNA.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLNA.G.E. column: 13
High quality sequence stop: 663.
Location/Qualifiers
                                                                                              510 TCTCCTCTGGACCCTGACTCGGGCCTCCTTTCATGTACTCTGCCCAACG-GTTTTGGGGG
                                                                                                              ACAATCTGGGCCAGAAGGGGAGCGCA - CTTGGCACCCCCTGATGCCAGCATCCTCATCAG
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AGENCOURT_8489704 Lupski_dorsal_root_ganglion Homo sapiens CDNA EQ898865 IG:22290891
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (asses 1 to 905)
NIH-MGC http://mgc.nci.nlh.gov/.
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Score 720.4; DB 13;
Pred. No. 2.4e-125;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.2%;
ilarity 98.4%;
Conservative
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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TITLE
JOURNAL
COMMENT
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ORIGIN
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                     481
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NotI; Site_2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5. TCGACCCACGCGTCCG-3' and
5. GACTACTTCTACATCCCACGCGCCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     946 GGGCTTCCGAGTGGCTTATAAGCGGCCACGTGCTGACCATGGATGACTTGGGGACCTTGTA 1005*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1006 TGGACAGAACTGGCTCAATGACCAGGTGATGAACATGTATGGAGACCTGGTCATGGACAC 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1126 TTATGATGGGGTGAAAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATCCCCATCCACCTGGAGGTGCATTGGTCCCTCATCTCTGTTGATGTGAGGCGACGCAC 1245
                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM13564 row: O column: 14
High quality sequence stop: 614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1066 AGTCCCTGAAAAGGTGCATTTCTTCAATAGTTTCTTCTATGATAAACTCCGTACCAAGGG 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TTATGATGGGGTGAAAAGGTGGACCAAAAACGTGGACATCTTCAATAAGGAGCTACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCTACAGGCAGAGGCGGTAAAGAAAGACCGACTGGATTTCCACCAGGGCTGGAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 29; Indels
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="Lupski_dorsal_root_ganglion"
                                                                                                                                                                                                                                                                                                                                                 /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
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                                                                                                                                                                                                                             Location/Qualifiers
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                   Unpublished (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 994)

S NIH-MGC http://mgc.noi.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gappa-remail.inh.gov

Tissue Procurement: Lou Stadat

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2062 row: m column: 08

High quality sequence stop: 620.

L. 9944
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                                                                                CAAACTICGICGGCAGAICIACAAGGAGCIGIGICACIGCAAACICACIGIGIGAGCCIC 1545
                                                                                                                                                                                                                                                                                                      ACTCCAGTICCTTTCCTCTTGCCTCTTCCCACTCACTT-CCCTTTGGTTTTTCATATT 1663
                                                                                                                                                                                           GTACCCCAGA-CCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAA 1604
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900
                                                                                                                                                                                                                     Length 994;
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/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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Pred. No. 1.3e-117;
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/db_xref="taxon:9606"
/clone="IMAGE:5812399"
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Homo sapiens cDNA clone IMAGE:6025493
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                              CCAGGGCTGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTG
                                                                                                              TGGTGCTTTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCAC
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Mismatches
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AGENCOURT_7770396 NIH_MGC_70
5', mRNA sequence.
BQ433698.1 GI:21172774
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Conservative
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JOURNAL
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13237 row. 1 column: 06

High quality sequence start: 41

High quality sequence stop: 300.

Location/Qualifiers

I. 936

//Organism="Homo sapiens"

//Organism="Homo sapiens"

//Clone=lib="IMAGE: 6025493"

//Clone=lib="IMAGE: 6025493"

//Clone=lib="MIHIMAGE: 70"

//Lone=lib="MIHIMAGE: 70"

//Lissue_type="epithelioid carcinoma"

//Lab_nost="MIHIMAGE: 70"

//Lab_nost="MIHIMAGE: 70"

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                                                                                                         301 GCAAGCATCTGGCCCTGTCTCAGCCATTCACCCCAGCAGGACATGCCCAAACTTC 360
241 AAATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCTTTTGTGTTGTGTACT 300
                                                                                                                                                                                                                      GACCCCAAGCCCATAAATGGGAAGGGAGACATGGGAGTCCCTTCCCAAGAAACTCCGTT
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/organism="Homo sapiens"
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/db_xref="hacks:4476128"
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Catarrhini; Hominidae; Homo.
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                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostor Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 715)

NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
659 CAGGAGCTTTTTCAGGGCTCAGATTTGGGCATGGCAGAAGAGGCAGAGAGGCCT-GGGGA 717
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10302 row: O column: 09
High quality sequence stop: 710.
Location/Qualifiers
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188 c 175 g 188 t
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Pred. No. 1.4e-116;
0; Mismatches 12;
                                                                                                                                      718 GAAAGCCGGCCAGCACAGCCCCTGCGAGAGGAGCA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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AL579669 LTI_FL012_TC1 Homo sapiens cDNA clone CSOBH007xF21 3 prime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 662) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                   1674 AATTTCTGTATTTTTTTTTTTTGAGAGAAATACTTGTTGATTTCTGATGTGCAGGGGGTG 1733
                               GGAGCAGTCATCCTCCCCCTTCCCCGTGCAGGGAGCAGGAAATCAGTGCTGGGGGTG 1850
                                                                                                                                                                                                                                                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 662
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/db_xref="taxon:9606"
/clone="comp00007YF21"
/clone=lbb="LTI_FL012_TC1"
/tissue_type="T_cells from T_cell leukemia"
/lab_host="DH10B"
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Catarrhini; Hominidae; Homo.
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                                   CCCTCATCTCTGTTGATGTGAGGCGACGCACCATCACCTTTTGACTCGCAGCGTACCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 676)
1960, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R.,
1.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessment of gene expression patterns in a model of metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
          Indels
          11;
ed. No. 3.9e-109;
Mismatches 11;
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BG870520 804 bp mRNA linear EST 29-MAY-2001 602791439F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922696 5', mRNA sequence.
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                                                                                                                                                      10;
                                                    Score 629.4; DB 10
Pred. No. 3.1e-108;
0; Mismatches 11;
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 167
Seq primer: Reverse.
                                                                                                                                                     31.6%;
98.1%;
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Best Local Similarity 98.1*
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Email: msoares@blue.weeg.uiowa.edu
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Seq primer: M13 Reverse.
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/Clone=_ib="NCI_CGAP_SG2"
/Clone=_ib="NCI_CGAP_SG2"
/Ib=_host="DH10B_(T] phage-resistant)"
/note="Organ: salivary gland; Vector: pcMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Dupublished (1999)
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. n. column: 09
Plate: LLAM10842 row: n. column: 09
Plate: LLAM10842 row: n. column: 09
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 804)
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                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="FVB/N"
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/u.cganism="Homo sapiens"
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/note="Organ: eps: Yector: pT713-Pac (Pharmacia) with a modified polylinker: Site_l: EcoR I; Site_2: Not I; ul=-bm0 is a cDNA library containing the following ul=-E-DM0 is a cDNA library containing the following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 626)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                        1417
                                                                                                                                                                                                                    1418 TTTGTGTTGCAGTACTGCAAGCATCTGGCCCTGTCTCAGCCATTCAGCTTCACCCAGCAG 1477
                                                                                                                                                                                                                                                                                                                                                                    GACATGCCCAAACTTCGTCGCCAGATCTACAAGGAGCTGTGTCACTGCAAACTCACTGTG 1537
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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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572
                                                                                                                                                                                                                                                                                                                                                                                                              TGGAAAGGTTACTTCAAAATGAATGTGGCCAGGCAGAATAATGACAGTGACTGTGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BM696661 626 bp mRNA linear EST 28-
UI-E-DW0-agk-m-22-0-UI.rl UI-E-DW0 Homo sapiens cDNA clone
UI-E-DW0-agk-m-22-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1538 -TGAGCCTCGTACCCCAGACCCCAAGCCCATAAATGGGAAGGGAGA 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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us-09-848-852a-4.rst

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sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                                                                                                                                    Query Match 31.4%; Score 626; DB 14; Best Local Similarity 100.0%; Pred. No. 1.3e-107; Matches 626; Conservative 0; Mismatches 0;
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Search completed: December 16, 2002, 17:45:56 Job time: 2574 secs